

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

ATGCGAAGCC GGTGCTGATG CCGAGCTCG CCGAATCGGT GACCGAGGGG ACCGTCATTC      60
GTGGGCTGAA GAAGATCGGG GATTGCGTC AGGTTGACGA GCCATCGTG GAGGTGTCCA      120
CCGACAAAGT GGACACCSAG ATCCCGTCCC CGGTGGCTGG GGTCTTGTC AGTATCAGCG      180
CCGACGAGGA CGCCACGCTG CCGTGGCGG CCGAGTTGGC CCGGATCGGT GTGCGTGGCG      240
AGATCGGCGC CGCGCGCGCC CCGAAGCCCC C
                                                                271

```

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```

Ala Lys Pro Val Leu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly
 1             5             10             15
Thr Val Ile Arg Trp Leu Lys Lys Ile Gly Asp Ser Val Gln Val Asp
      20             25             30
Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro
      35             40             45
Ser Pro Val Ala Gly Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala
      50             55             60
Thr Val Pro Val Gly Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Glu
      65             70             75             80
Ile Gly Ala Ala Pro Ala Pro Lys Pro
                        85

```

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

GAGGTAGCGG ATGCCCCGAG GAGCACCCCA GGACCGCGCC CGAACCGCGG GTCCCCGTCA      60
TCGATATGTG GGCACCGTTC GTTCCGTCCC CCGAGGTGAT TGACCAT
                                                                107

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

ATGAAGTTGA AGTTTGCCTG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCCTTTGTG      60
TTTCCTGCCT CGTTGCCAG CGCAGATCCA CCGACCCCGC ATCAGCCGGA CATGACGAAA      120
GGCTATTGCC CGGTTGCCG ATGGGGTTTT GGCGACTTGG CCGTGTGCGA CCGCGAGAAG      180
TACCCCGACC GCTCGTTTTG GCACCACTGG ATGCAACCGT GGTTTACCGG CCCACAGTTT      240
TACTTCGATT GTGTACGGG CCGTGAGCCC CTCCCGCGCC CCGCCCCACC GGGTGGTTGC      300
GGTGGGGCAA TTCCCTCCGA GCAGCCCAAC GCTCCCTGA                               339
  
```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1           5           10           15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 20           25           30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35           40           45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50           55           60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65           70           75           80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
 85           90           95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100           105           110
  
```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTGACCACCG	TGGGCGTGCC	ACCAACCGCG	GCAGCGGCAG	CCGCGCGCGC	GCCGCGCGCT	50
CCGCGCGCAA	CGGTGGCGCC	GGGGTAAACG	CCACCGGCTC	AGGCGGCAAG	GCGCGCGGCC	120
GTGGCAATGG	CGGTGATGGG	AGCTTCGGCG	CTACCAGCGG	CCCCGCGTCC	ATCGGGGTCA	180
CGGCGCGCCC	CGGCGGCAAC	GGCGGCAAGG	GCGCGCGCCG	TGGCAGCAAC	CCCAACGGCT	240
CAGGTGGCGA	CGGCGGCAAA	GGCGGCAACG	GCGGTGGCGG	CGGCAACGGG	GCGTCGATCG	300
GCGCGCAACG	CGGCATCGTC	GCGGTTCCG	GTGGGCGCGG	TGGCGCTGGC	GCGCGCGCGC	360
GAAACGGCAG	C					371

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC	CACCACCGCG	CGGCGCGCGC	CTAGCGCGCC	GGCGCGACCA	GCCCCCTTTC	60
TTCACCTGTT	CAAGAAAGG	GCCTTCGTGT	TGGTCGGCCA	TGTTGGCATG	ATCGTGACCC	120
ATGGGCAACA	TGCACCTCGA	CATCTCGGCC	AAGGTCTAGC	TCCATGCGAA	TGCGCGCGCG	180
GCTGGTGAGC	ATCGGTCTAG	CGGTCTATAG	AGGCTTCGCG	GTACCTGTTC	CCGACGCACA	240
CCCGTCGAG	CCCGGGGTG	TGTCTTACCG	GCTGCTCGGA	AAGGGTTCGG	TGCGCAACAT	300
CCTCGGCGCC	CCAATGGGCT	GGGAGGCGGT	GTTCAACCAAG	CGGTTCGAGG	CGTTTGGGTT	360
CGAATACCG	GCCTGCAACA	ACTGGGTGGA	CATCGGGCTG	CCCGAGGTGT	ACGACGATCC	420
CGAC						424

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GCGATGCGCG	CGCGCGGTAC	CACCCGCAAT	GTGGAAACGT	TTCCCAACCG	CAACGATGCT	60
TTCATCTGCG	CGTCAATTGA	CTTCAGCGCG	GCCGATTTCG	TCACCGAGGG	CCACCGTCTA	120
AGGGCGGATG	CGATCTACT	GCGCGGTACC	GACCGGCTGC	CTTTCGCGGA	GCGCGCGGAT	180
TGGGACTTGG	TGGASTGCGA	GTTGCGGACG	ACCGTCACCG	CGGACACGGT	GCGCATCGAC	240
GTCATCGCGG	ACGATATCGG	TCCGGAAGTG	GCGCGGGGCT	CCAAACTCAC	CGAATGCGCTG	300
CGGCTCTACG	ATTGCTC					317

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCCGC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTGGATCAGC	ATCGCAGTGT	GCCGTTCGTG	ACCGACACCG	CGSTCCAACG	120
TGAAGTGAGG	GCGGAAATC	GCGCGAAATC	TGCGCCCTCAG	TTCAAGCTCG	GCGCCTAACG	180
GTTCTGGGAG	TTGGGTGCGC	GCTTCTCGGC	GAACGCGCGC	GCGCCTTCCT	TGGCTCTGTC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTGGATCTTG	AACGCTCGT	TTTCGGGCAT	300
GCACTCGGTC	TGGCGGATGG	ACCGCAGAT	GCGCTGCAGC	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCC	GCAAGTTCTA	GAACCTTGGT	CAACGCTCTG	CGGTCCGGCA	CACGTGCGCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GCCTGCCGCT	GAACACCAGC	CGCGGCTGC	CAGATCTCCC	GGACTCGGTA	GTGCGCGCGG	60
TGGCGTGGTT	GCTCTCTGTA	CGGGGCGCGG	CGACCATAAG	GTGCTAATG	CCGAGGTAGC	120
GGCCGAGGTG	CATCGAGTGC	ATGATGATGC	GACTCTCCAG	CTGCGCGACC	GGGAGCTTGG	180
CATCGGSCCT	GATCAGCCAG	GACGCGTAGG	ACAAGTCGAT	CGAATGCATA	GTGGCCTCCA	240
GAGTGGCGGT	GCCACTTCCG	GCTGCTCCA	CGGCAATGCG	CTTGATTCT	AGCTCCGCGT	300
AGTGTTCGCG	CATCGGCTGC	GGATGAATG	GGAACCGCAG	GATGGCGACA	AACGGSTCTG	360
ACCTCAGGTT	TGCGGCTTGG	CGCAGCTGG	TGGACAGCGG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGGCGA	GGGTGTGCTC	GCTGCCGCGG	GCAATGTGCA	TAATGTGCGC	TGGGTGAGCG	60
CGCCGATCAA	CTAGTGAGGC	GCAACGCTAG	GCTTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCGGC	CTACGCGCGC	ATGTGCGGGA	180
CGGAACCCCT	GACCAAGACC	ACGATCACCC	GTGCGGAGCC	GGGCGCGCAC	GACATGGCGA	240
TGGACATCAA	ATTGCGCGGA	ATCTGTGCGT	CGGACATCCA	TACCTTCGAA	ACCGAATGGG	300
GGCAACCGAA	TTTACTTGTG	GTCCCTG				327

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1             5             10             15
ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
      20             25             30
Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe
      35             40             45
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
      50             55             60
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
      65             70             75             80
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
      85             90             95
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
      100             105             110
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
      115             120

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1             5             10             15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
      20             25             30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
      35             40             45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
      50             55             60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
      65             70             75             80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ala Ser Lys Leu Thr
      85             90             95
Glu Ser Leu Arg Leu Tyr Asp Ser
      100

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1             5             10             15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
      20             25             30
Ala Pro Thr Pro Pro Ser Asn Val Asn
      35             40

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1             5             10             15
Val Pro Pro Val Ala Ser Leu Leu Ser
      20             25

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1             5             10             15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
      20             25             30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
      35             40             45

```

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGCC	CTGGAGCGAC	GGTGTGGGTC	TGGGGGTCCA	TTCTTCTCC	GCGAAAGTCA	50
ACTAAGAGAC	ACGTTGACAC	CCAACCGGCG	GCCCGGCATG	GCGCGTCCCG	GCGTAGAGAGC	120
TTTGACCGCG	GCGCGAAGCG	TTCTCTGCTG	CGCGCCATGC	AGATCCGACA	CGCTTCTTTC	180
AACATCGGGT	GGAGCCCGTG	GTAACGCCAG	GCT			213

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCCGCCCC	GCGGTTCCCG	GCGGCGCGGG	TGGGCGCGGC	ACCGACCGCG	50
GGCCCCGTGC	TACCCGCGCG	ACCGCGCGAC	ACCGCGGAGT	CGGCGGCGAC	GCGCGATGGC	120
TGGCACCOCG	CGGGGCCCGC	GCGGCCCGCG	GGCAAGGCGG	GCGAGGTGGT	GCCCCCAGCG	180
ATGCTGGCGC	GTTGGGTGGT	ACCGCGCGGA	CGGCGCGTAC	CGGCGGCGCC	GTTGGCGCGC	240
GCGGTGCGCG	CACACTGCTG	CTGGGCGCTG	GCGGACAGGG	CGGCTTCGGC	GCGCGCGGCG	300
GACAAGGCGG	CACCGCGCGG	GCGCGCGCGA	GATGCGCTTC	TGGGGGGTGT	CACTGGCACT	360
GGTGCTA						367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGGGTGAT	TGGCAAGGCG	ACCGCGCGAC	GCGCGGTAGC	CGCGGGACCG	CCGAGGCCCC	60
GACCGCAGCG	GCGGTGTCT	GACCGGGTCA	GCGACGAGCG	GCGGTGACCG	TGCGGCTCTT	120
CTACTTGGAC	CGCAGCGGCT	TCTCAAACT	TCTCACCACC	GAGACAGGGA	GCTCGCTGGC	180

```

GTCCGCTCTTA TGGGACCGCT GCGACGCGGC ATTGTCCAAC CGCTTGGCCT ACCCGAAGT      240
CGGCGCGCGCA CTCGCTGCAA CCGGCGCGCA TCACGACCTA ACCGAATCCG AGCTCGCGCA      300
CGCCGAGCGT GACTGGGAGG ACTTCTGGGC CGCACCGCGC CAGTCGAAGT CACCGCGACG      360
GTTGAACAGC ACGCGCGGCA CTCGCGCGA ACACATGCTT TACGCGGAGC CGACACCTT      420

```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

CTCTTTGTGG TGGCATCGGC GGTACCGGCG GAACCGGCGG CACGCGCGT ATGCTCGCGG      60
GCGCGCGCGG GCGCGCGCGT GCGCGCGCGT TCAGCTTCAG CACTGCGCGT GCGGCTGCGG      120
GCGCGCGCGG GCGCGGTGGG CTCTTCACCA CCGGCGGTGT CCGCGCGCGC GGTGGGCGAG      180
GTCACACCGG CCGGCGCGGC GCGCGCGCGG GCGCGCGCGG GTTGTTTGGT GCGGCGCGCA      240
TGGGCGGCGG GCGCGGATTG GCGGATCAG GAACGCTCGG CACCGCGCGG GCGGCGCGG      299

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
1           5           10           15
Ala Lys Val Asn
20

```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
1           5           10           15
Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly

```



```

                20                25                30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
   15                40                45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
   50                55                60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
   65                70                75                80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
                85                90                95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
                100                105                110
Ser Gly Gly Cys Gln Trp His Trp Trp
                115                120

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1           5           10           15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20           25           30
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1           5           10           15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
 20           25           30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
 35           40           45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50           55           60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65           70           75           80

```

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTGTTCGG	CGCCCGCCGG	GTGGCCGCTG	TTGGCCGCTGA	CGGTGTGGCA	TTCTGGGCA	60
CGGCCCCCGG	CGGCCCCCGT	GCTGCCCGCC	GCGCCCGCTGG	GCTGTTCAGC	GTCCGTGGGG	120
CCGCGCGCGC	CGCCGGAATC	GGATTGGTCC	GGAACAGCCG	TGCCCGGGGG	TCGCGCGCGT	180
CGGCCCCGCT	CTGGGCGGAC	GGCGTCCCG	GCGCCCGGGG	TGGGTCGGG	TCCACTACCG	240
CGCGTGGCGG	CGGCGCGGGC	GGCAACGCCA	GCCTGCTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCAAGAGC	CGTGGTACTG	GTCAACTGAT	GGCCTGATTG	TGACCTTCCC	GGCSCCGGAT	60
CAGTGCCTTC	CAGGACCGAC	GTAATATTCG	AAAACCAATC	CGGCCCGCGA	GGCGAGGATG	120
AATGCCACAC	CGGCGCGGAT	CAGCCACGGG	AGCCACAACG	CGATGCCGAC	CGCTGCCACC	180
GAGCCCGACA	ACGCGACCAT	GATCGGCCAC	CAGCTATCCG	GACTGAAGAA	TCCAAGTTCT	240
CCTGCGCCCT	CGCTGATTTC	AGCSCCTTCG	TAGTCCTCGG	GGCSCGAATC	TAACCGCGCG	300
GCCACAAACC	GGAAGAAGGT	GGCGACGATC	AACGCCATGC	CGCCGCTGAG	CGCCAACGCA	360
ATGGTGCCAG	CCCACTCGAC	ACCACCGCTG	GCGAACATCG	AGGTCAACAC	GCCGT	415

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TCACCCCGTG	AACGGTTCCT	AACACTGATA	CGTATGCTTG	TCACCGAGCA	GATCAAGTCC	60
AGTCCGACCA	ATGCCAGGAG	ATCATCGGCT	AGGCTCAGCG	TTTCGGCTTG	GACGAGACGG	120
TATTCAGTTC	TGGCGTTGGA	CGGTCCGTGG	CGTGGTGGGA	AGTCTGACGC	GGCATCAGAA	180
CGGTTGTCAA	TACCACTCTT	TGGGGGATAT	GGCCTATTTG	GTGTCTCGG	GGCGCTCCAC	240
CGGATCCCTT	TTGAAACGTT	GGSCAAGGCG	GGTCCAGTTA	CGGCTCTTTC	ACTGCGCGCT	300
GGGCTAGCTG	CGCGGCGTCS	ATCGGTTTGA	ACSTCATCGC	AATTCGCGCA	ATGGGTGAGT	360
ACCTGACGCT	CCY					373

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGGA	CAGGCGGCA	GCGACGCTCS	GAAGTTGCAC	CACGGTCCGC	GCTCCATGTA	60
GCCAAACGGT	GACCAAGCGG	TAGACAGCAG	ATCCGTGGAT	CGCGCGTTCC	GTGTCTCGG	120
GGCCGASTAC	CGCGCGGCGG	AACCGCAGCG	ACCAAAGCAA	CGCATCGAT	ACGGGGATCG	180
CCACTCGTGC	CGAATTCGAG	CTCCGTGGAC	AAGCTTCCCG	CGGCACTCGA	ACCCGGGTGA	240
ATGATTGAGT	TTAAACCGCT	TAGCAATAAC	TAGCATAACC	CCTTGGGGCC	TCTAAACGGG	300
TCTTGAGGGG	TTTTTCTG	AAAGGAGGAA	CTATATCCCG	ATAACCTGGC	GTAGTAGCGA	360
AGAGGCGCGC	ACCGATCGCT	CTTCCCAACA	GTTCCCGCAG	CTGAATGGCG	AATGGACGCG	420
CCC						423

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGGZAGC	CGGTCCGCCA	ATGCATCCAG	CTCCCGGTAC	GTCAAGTGAC	CATCCGCCCCA	60
ACTGACCGCC	ACCGACTCAG	GCTGTGCGGC	AGCGATTTCC	GCGAACCGGG	TATGACCGGC	120
GGGTGCGGAC	GTGTCACAT	CCGGCAGGCG	GGGTGCGGTC	GGATCGTGCT	CGCGCTCCAG	180
CAGAATGTCC	ACGTCCGCKA	GCGGCGGATC	CCACCGGCTG	ACCAAGCGCT	GTAACACAGC	240
CAGCACCGGC	CTGCGGAGGC	TTTCGGGCGC	CATCGTGCGC	AGCGCACCTT	CGAGCACCTC	300
CAGTACGAGC	GTGAGCTCAC	CGGTGCTGCG	GTGCGCGCGC	ACGCTCACCG	GAAAGTGCGA	360
CAAACTCTCT	AGCGCCACCG	GACGGAACCT	CACCCCGTTT	GCGA		404

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCTCTGGTGG	CAGGCTGTTC	TTGGAACCCG	CTGGCTAACT	TGGACCCCGG	GTATCCGCCC	60
ACCATCGAAC	CGGCCCAACC	GGCGGTGTCA	CGCCCTACTT	CGCAAGACCC	GGCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCC	ACAACGGCAC	CGGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCG	CGATTGGGCG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCCG	CAGCCGCGTT	GACCAAGGAC	300
GACCAAGGCA	CGGCTTCTT	TGCCCGCCG	GGCGCTACT	TGGTGGCGCA	CCTGTCTCTC	360
GGTCACACCG	CACGAGTGAA	TGTGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACGC	CATCTTGGT	GGGATCTTC	GGGCGGGCGG	CAGTGAACCTA	60
GACGAGCTGC	GGCGCTTCAT	TCCGCGTTGG	GTCAAGCTGG	GCTCGGCGCT	GGCGGCGCTA	120
CCGAAAGCCA	AACCGGACTA	TGGCGGCTTT	AGCGCGTGGG	GCGGCGTGGC	CGAGTGGCGG	180
CGCGAGTAGG	ACACTGTTCAT	CGACGAGCTC	ATCGAAGCCG	AGCGGGCGCA	CCCGAACTTC	240
GGCGATCGGA	CGACGTTTTT	GGCTTGTATG	CTCGCGAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTGCGSCA	AGGACATTGG	CGACGAAGTG	CTCAGGCTGC	TTGCGGCGCG	GCACGAAACC	360
ACGGCGGGCA	CATGGGCTGG	GGCTTCGAAC	GGCTCAACCG	GCACCCCGAC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCTCTGGTGG	CAGGCTGTTC	TTGGAACCCG	CTGGCTAACT	TGGACCCCGG	GTATCCGCCC	60
ACCATCGAAC	CGGCCCAACC	GGCGGTGTCA	CGCCCTACTT	CGCAAGACCC	GGCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCC	ACAACGGCAC	CGGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCG	CGATTGGGCG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCCG	CAGCCGCGTT	GACCAAGGAC	300
GACCAAGGCA	CGGCTTCTT	TGCCCGCCG	GGCGCTACT	TGGTGGCGCA	CCTGTCTCTC	360
GGTCACACCG	CACGAGTGAA	TGTGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420

CGCCCTCCG ACGGCAAGCT GGTGCTGGGC AGGCGAGATG GCGCCCTCTA CACGCTTGCC 480
AAGAACCCCG ASTTGACCGG CGTCGGGGCC GCCACGCTAG CC 522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGGCC	ACGCGCGTCC	GGGGGGCCCA	GCCCCCTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGCGCGCC	CCGTCTGTCT	CGTCTCTCTG	TTGGGCGCCA	120
TGGGATCTG	GATCGCCATC	CGGCCCCAAGC	CGGTACAGCC	GCTTCAGCCG	GTTGCGGAGG	180
AGCGCCTTAG	CGCCCTACTG	CTGAAGTCTT	CAGAAGTCAA	CGCCGTGATG	GGCTCGTCTT	240
CCATGCGGCC	GGGCAAAACCG	ATCACATCGA	TGGACTCTTC	GCCGGTGACC	GTGTCCCTGC	300
CGGACTGCCA	GGGCGCGCTG	TATACGAGCC	AGGATCCGGT	GTATGCCCGC	ACCGGCTACA	360
CGCCCATCAA	CGGCTTGATT	TCATCCGAGC	CGGCGGACAA	CTACGAACAT	TGGGTGAACC	420
AAGCCGTCTG	CGCCTTTCCG	ACCGCCGACA	AAGCCCGCGC	GTTCTGTGAG	ACTTCGGCCG	480
ACAAATGGAA	GAAGTGGCCA	GGCAAGACCG	TCACCGTCAC	GAATAAGGCT	AAGACTTACC	540
GGTGGACGTT	TGCGGACGTC	AAAGGCGAGC	CGGCGACGAT	CACGCTGATA	GACACCCAAAG	600
AAGCGCTGGA	GGGCTGGGAA	TGCCAAGCGG	CGATGAGCGT	GGCCTAACAT	GTGGTTGTCT	660
ACGTCAACGC	ATGCGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAAGATCT	720
GTTGACAAAG	TCACCAAGG					739

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGACGTCTTC	GGGGCCGCCA	TGGCCCGCGC	CGAAGCCGTT	AACCGCGCAC	TGAACCGGTT	60
GGCTATGCG						69

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGCAACCCG	GCAGGCGCGA	CCAACCGATC	GESTCAACTA	GCACCTGCCG	TGGAGGCGCC	60
CCCGCGCTCT	GTGCGCTCCC	ACGCGGAACC	CTTGGGCAGC	GCGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTC	GACGACCGTA	TGACAGAGCG	GTTCCCGGTC	TTACAGCTCG	CCAGTCTCCG	180
CGAAGCGCTG	CCGGGTCCGC	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGGACTGCG	240
CCCGCGCGGT	CGGCGGATGG	GTGCGGTACT	GCGGCTTGCC	GCTGTCCTTG	CCGATGAGTG	300
CGAGAGAAGA	GCCATCGCGG	TGTTGCGTCA	CCGCGCGTAT	ATCGGAGTGT	CGGCGCAATAT	360
TGTGCGCGCC	GCCCAACTGC	CGGCGTGCGA	CGCGCAGGCC	GTACCCCGGC	GGGCACTGCG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTTGGTCCG	CCGCAACTTG	CGGCGCGACC	480
GCTCGGCTCG	GTGCGGAAGG	TGTCGTGAC	GGCACGGTCG	CTG		523

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTCGGTGT	CGTCGGGCTA	GGAGCGACTT	CCCCCGCCCG	CGCCCGCGCC	GGAGCGGGCT	60
GTGCGGAAC	CGGTGCGGCG	GCGGCGCGCG	GGCGGACCGA	AGGCGCGATC	GATTGCGGCA	120
CGGCTTGGCT	CGCGGCTTGG	TGACCGCGGT	TGTTGGCGGT	CGGAGCGCAT	ACCACGAACC	180
AACGCTGAAG	GGGCGCGCGG	TCCGCTGCTT	TGCGCGCGCG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAAGTGAAT	GCGCGGCTCG	ATCGCGCGCG	GCGGCGGTCT	ATAGCTGCGC	CGCCAGGCTA	60
TGAAGTGAAT	TTGCGCATAG	CGGCGGCTTG	TGTCGGGCTT	GTCCAAACCC	TGCGCGCGCG	120
CTAGTGGCG	TTGCTTGAAC	CGCCAGCTAC	GCGGCGCGCG	AATCCAGAGC	CGATCGGCGC	180
TGTCGAACCG	CAGATCGCGC	GTGGTGAATC	CGCGCGCGCG	CGACGAGGTC	TAGAGCACCT	240
CGGCGCAATG	GTGCTGTTCC	GCGATCAGCT	CGCGCGCTTC	AACCGGCTCT	GCTTGGGCTT	300
TGTCGCTCAG	GCGGACATCG	ACCGAGCGCG	TGAACAGGTT	GAGGCGATTC	CAGTGGGCTT	360
CGCGGCTGCG	CAGCAACGCC	AGGCTGCGCG	TGTTTGGCAT	ACCGGCAAGT	CTCTCAGGCA	420
CTCCGCGACT	GCTCATCGTG	GACCAAAATG	CGCGAATTC	GCTGCGTCCG	CTGCGCGCGC	480
CGTTCATACC	GCGGAGGTGG	TGCGGACCGT	AACCGGCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC	ATTGCTCTGA	ACAAAGCCAC	CCGCCCCGTAC	AGCGGACGCC	CCCATTCGTT	60
GTCTGTATAG	TCGCGGTACA	GCTGGGCATC	GGCCCCCTGGA	CGAAGCTCCG	CCGAGGGGCA	120
GGGAACGAGC	CCGTGCGGSC	TCACGCGGGG	TCAGAACGGT	AGTGCACGAC	AGTCTGCCCC	180
CGGNAAGGGT	TTGACCGGTC	AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGGCG	CTGAGCTCA	CGGCCGAGCC	GTTCAGCAGC	CCAGTCCACC	300
TCGCTGGTCT	TGTTCCCGCG	CAGCAGCTGC	GTGAACCTGA	CCGCTCGAC	ATCGGCGCGG	360
GTGACCCCGA	ACGCGCGCAG	CGTCGTGCGC	GTGCTGCGCC	GGCGCAGGGG	CGGCAACTGC	420
TCGCCA						426

(2) INFORMATION FOR SEQ ID NO:275:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:275:

CGCGACACGG	CGGACAAAGC	GCATCGGCC	TCGGCGGCGG	CGCGGCGCGC	GACCGGGGCC	60
AGGGCGGCGC	CGGGCGCGGA	CTGTGGGTA	CTGGCGGCGC	CGCGGACAC	GGCGGGSCAA	120
GGCGGTGGTA	CGGGGGGCTT	ACCGCTGCCC	GCTCAGGCAG	GCATCGGCC	CGCGGTGGC	180
GGCGGTGGGC	TGATCGSCAA	CGCGGGGCTT	GGCGGCGAC			219

(2) INFORMATION FOR SEQ ID NO:276:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG	GGCGCGCTCC	TTAGCATGSC	TCGCTCTGSC	ATCGTGGCCC	GGCGGATCA	60
CGGAGGTCCG	GCCTTGATCC	CCACTGCTCG	AACGGTCAGC	ACCACAGTCG	GGTTCTCGGG	120
ATCCTTTTCC	ACCTTGGCCC	GCAGACGCTG	GACATGCACG	TTCACTAGCC	TGGTATCGGC	180
TGGGTGCCCC	TAACCCGATA	CCTGTTGAG	CAGCAGATCA	CGAGTAAACA	CCTGGCGCGG	240
CTTGCGCGCC	AATGCGACCA	ACAGTTCGNA	TTCCAGCGGT	GTCAACGAGA	TCTGCTCACC	300
GTTGCGAGTG	ACCTTGTGCG	CGGTACGTC	GATTTCTACN	TCGGCGATGG	ACAGCATCTC	360
GGCGGGTTCC	TCGTGTTTC	GGCGCAGCCG	CGCCGCGACC	CGCGCAACCA	GCTCTTGGG	420
CTTGAACGGC	TTGATGATGT	AGTCGTGCGC	GGCGGACTCC	AGAGCCAGCA	CCACATCCAC	480
GCTGTGCGTC	TTTCCGCTGA	GCATCAGGAT	CGGAACACCG	GAATCGGCGC	GCACACCCG	540
GCACAGCTCG	ATGCGGTTCA	TACCGGGGCA	A			571

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1           5           10           15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
 20           25           30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
 35           40           45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
 50           55           60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
 65           70           75           80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
 85           90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1           5           10           15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
 20           25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

235

```

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1           5           10           15
Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
      20           25

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1           5           10           15
His Pro Pro Asn
      20

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
      20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
      35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
      50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
      65           70           75           80
Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
      85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
      100           105           110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
      115           120           125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
      130           135           140

```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
 20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
 35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
 50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
 65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
 85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
130          135          140

```

(3) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro*Ala Ser Ile Met Val Phe Asp Asp
 65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
100          105          110

```

237

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Gln His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

238

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1           5           10           15
Leu Asn Ala Leu Ala Tyr
                20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1           5           10           15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
                20           25           30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Gln Phe Asp Asp Arg Ile Asp
                35           40           45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
 50           55           60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65           70           75           80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
                85           90           95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
                100           105           110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly
                115           120           125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
                130           135           140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
 145           150           155           160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
                165           170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

239

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1           5           10           15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
 20           25           30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
 35           40           45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1           5           10           15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
 20           25           30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
 35           40           45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
 50           55           60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
 65           70           75           80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
 85           90           95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln
100           105           110
Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Ile Glu
115           120           125
Arg Gly Ser Gln Phe
130

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1           5           10           15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
          20           25           30
Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
          35           40           45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:290:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1           5           10           15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
          20           25           30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
          35           40           45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50           55           60
Arg Gln Arg Arg Gly Arg Arg Arg
 65           70

```

(3) INFORMATION FOR SEQ ID NO:291:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
          20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
          35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60

```

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CCGCACGTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG	60
CGAACGGTTA TTGACGGCCC GGAGGGCACT CGGCTGCCAC CAGCTGGTGA CTCAGCGCGT	120
TTTCACGGCA ACCAAGCGCG GACACACCAC TTGACATTC ACAGCACGGC CCGG	174

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TGGCAAACGG GGTACCTTC CTTCCGGTGG CGCTAGAGAG TTTGTCCAC TTTCCGGTGA	60
CGGTCCGGCC GCACCCACAC ACCGGTGAGC TCACCTCTCT AGTGGAGGTG CTCGACGGTG	120
CGGTGGGCAC GATGGCGCCG GAAAGCTTCG GCAGCGCGGT CTTGGCTGTG TTACAGCGCT	180
TGGTCAGCCG GTGGGATCGG CCGCTGCGCG ACCTCCACAT TCTGCTGGAC GGCAGACACG	240
ATCCGACCCG ACCCGGCGTG CCGGATGTGA CGACGTCCGC ACCCGCGGTG CATACCCGGT	300
TCCCGGAAAT CGGTCCGGCA CAGCTGACT CGGTGGCGGT CAGTTGGCGG GATGGTCAGC	360
TGACCTACCG GGACCTGGAT GCATTGGCCC ACCGGCTGGC CACT	404

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His	
1 5 10 15	
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu	
20 25 30	

242

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 15 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(3) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTCGAGCG	CTACCACTAC	CTGTTCTGGG	TGGTTTGTGC	GCGCGCTTAC	GACGACAAGG	60
CCAGAAGAC	CACCAAGGCC	GTGCGGAGGC	TGTTGGGCTT	CGCGGGGCTG	AAATACTTGG	120
TGCTGGGCGC	TGGGAAACCT	TGCAACGGCG	ACTCGGCGCG	CGGCTCCGCG	AACGAGTTCC	180
TCTTCAGCA	GCTGGGACAA	CAGGCGCTCG	AGACCTTGGG	CGTTTGTTC	GAGGTTGTGG	240
AGACCTTGGG	CGCAAGATC	GTGTCACCTT	GCTCGCACTG	CTTCAACACC	ATCGGCAAGG	300
AATATCGGCA	GCTGGGCGCC	AACTACAGCG	TGCTGCACCA	CACCGAGCTG	CTCAATCGGT	360
TGCTGGGCGG	CAAGAGGCTG	GTGCGTGTCA	CTCGGTTTTC	TCAGGACATC	ACCTACCAAG	420
ACGCTGTGTA	GCTGGGCTGG	CACAACAAGG	TCTACGAGGC	ACGACGGGAG	CTGATCGGTC	480
CGCGGGGGCG	CACTTGAGCC	GAGATGCGCG	GCCATGCGGA	CCGCGG		526

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCGCGGCGG	TGATCTGGCG	GCGCAACTTC	GTCACTGCAT	CGAGACCCCA	ACGATCATCG	60
ATCAGGCGCG	TGCCCATGAT	CACCGGACCG	GCCACGAGCA	CGCGGGGCTT	GCGGTTGGAA	120
TAGACGAACC	CCCGGCTGAG	TGCGGGAAGC	TGGGAGGCAA	GAAAGACGCG	GCCGACAAATG	180
CCGAGGAACA	TGCGCAACCC	ACCCATCCGA	GCGGTAGCGG	TGACGTGCAC	ATCTCGCTCC	240
CGCGGTTAGG	CGACGGCTCC	CAGGCGACTG	GCCAGCATCC	GCACCGGACC	GCTCGCAAAA	300
TAGGTGATGA	TGCGCGGCTT	CAGCGGAGCT	AGCGGAGCTT	CAGCGGCGCG	GACACTGGCG	360

CCCGGATAGG ACAGGGGCGAG CAAGCCACCG GCAACGGCGG CCACATCGCT GGACACCTCG	420
AGACCGTACT GCACCAACTT GAAGAGCTGA ACACTGGCGG AACGTGCAAC AGCTGCGAAC	480
AATTGGG	487

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATSTA CGAGCTTGAG TTCCCGGCGC	50
CTCAGCTGTC GTCTGCGAC GCGCTGCTC CCGTGTGGT GCACGCTTC GAAGGTTTCT	120
CCGACGCGCG CCATGCGATC CCGCTGGCGG CCGCCCACT CAAGGCGGCG CTGGACACAG	180
AGCTGGTGG GTCTTCGCG ATCGATGAAC TACTGGACTA CGCTCGCGG CGGCCATTAA	240
TGACTTTCAA GACCGATCAT TTCACCACT CCGATGATCC TGAGCTAAGC CTGTATCGCG	300
TGCGCGACAG CATCGGCACC CCGTTCTGC TCGTGGCGGG TTGGAGCGG GAGCTGAAGT	360
GCGAGCGGTT CATCACGCG GTCCGATTC TGGCGGAGCG CCGCGTGTG CCGCAGAAC	420
ATCGCGCTGG GCACCTGCT GATGCGCTT CCGCACACAC GACCGATCAC GATGACTGCT	480
CATTCCAACA ACCCGGAGCT ATCTCGATT TTCAACGTT CGATCTCC	528

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAGCGCGCT CAAGGAGCGG GTGCGCGCT TCGCTCGCT GCGCGCGAG CCGCGCTTC	50
CGCGCTTTCG GCGCTTTCG CCGTACCGG GCTTTCCTAC GGTGCGCGG CCGCGCGCA	120
TGCGCGCGCT GTTAGCGCG TTTTCGCGG CCGCGCGCT ACCGCTTTC CCGCGCTTC	180
CGCGCTTTCG GCGCTTTCG GCGTTCGCG CCGCTTCGAC GTATTGTTTC ACCGCGCTTC	240
CCCTTGACCG TTGCGCGTG TCGATCGCG CCGTTCGCGA TCGCGCGAC ACCGCTTCG	300
AAGCTTCGCG TGCGCGCGCA GCGCTTCAC TGTGTCGCG CCGCTTCGAT TCGCGCGCG	360
CGACCGAGAT GATGCGCAC ACCGAGCGT GCGCGCTTC GCGCGAGCG AGCGCGGTT	420
CGCGCTTCAG CCATACCGCA CCGTTCGCG CCGCTTCGCA GATTTCAGG CTGCTTCGCA	480
CGAGATCGAG CAGCGGTGT CCGCGGACT GCGTTAGCG GTTTCGCGG CCGCTTCAG	540
GGCGAGCGCA ATATCGCTG CCGCTCGAC CAACCGCGC TCGATAAGG ACACCTTCG	600
CGCTTCGATG	610

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid

244

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1           5           10           15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
 20           25           30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
 35           40           45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
 50           55           60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
 65           70           75           80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
 85           90           95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
100          105          110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
115          120          125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
130          135          140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145          150          155          160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

```

245

```

      100      105      110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
    115      120      125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
    130      135      140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
145      150      155      160
Leu

```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Gln Leu Glu
 1           5           10           15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
    20           25           30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
    35           40           45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
    50           55           60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
    65           70           75           80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
    85           90           95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala
    100          105          110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
    115          120          125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
    130          135          140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser
145          150          155          160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
    165          170          175

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1           5           10           15
Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20           25           30
Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35           40           45
Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50           55           60
Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65           70           75           80
Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85           90           95
Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg
100          105          110
Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
115          120          125
Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
130          135          140
Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
145          150          155          160
Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
165          170          175
Pro Leu

```

(12) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

AATTGGGCAC GAGCAGCACC AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA      60
TCGGCAACAC CGGCAGCTTC AACACCGGCA GTTTCATCC GGGCGATTCC AACACCGGGG      120
ATTTCAACCC AGGCAGCTAC CACACGGGGA CTCGGAAACA CCGGCGATTT TACACCGGCS      180
CCTTCATCTC CGGCAGCTAC AGCAACGGGT CTTGTGGAGT GGAAATTATC AGGGCTCATT      240
GGTTCACCCC GGGCTTTCGA ATCCTTCGAG CCAATTCAAC TCTTCACAAA GTTTGCGGCC      300
GCACTCSAGC CCGGTTGAAT GATTGAGTTT AACCGCTNAN CAATAACTAG CATAACCCCT      360
TGGGGCCCTCT AAACGGGTCT TGAAGGGTTT TTTGCTGAAA GGANGAATA TATCCGGATA      420
ACTGGCCGTAN TACGAAAGGC CGCACCGATC GCCTTCCCAA CAGTTGCCCA CCGGAATGGC      480
AATGGACCNC CTTETTACCG GGCATTAAAC CCGGGGTGTN GGGTTACCC CCACCTNACC      540
GCTACCTTGC CANNSSCTN RSGCGTCTT TCTTTCTTC CTCCTTCTC CCMCTTCGCC      600
GGTTCCCTTC AGCTCTAAAT CCGGGNNCC TTTMGGGTTT CAATTATTGC TTACNGSCCC      660
CCACCCCAAA AAYTNATTNG GGTTAATGTC CCTTMTTGGG CTTCCCCCTA WTNANNGTTF      720
TCCCCCTTNA CTTTGGSTCC CTCCTTTATW NTGAGCTNT TTCCACYGGA AAAMNCTCCA      780
CQNTTYSSES TTTCTTPGA WTTATMRGR AATTSCAATY CCGCTTTEGG TTMAANTTAA      840
CTATTTTCA ATTTTCCCGM TTTTMMNATR TTNENKCGM KNCTCCNKA SSGNTTTCCT      900
CCCCCTTSS GKTYCCCCN G

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCGGCAC	GAGATANESG	GGCACCGGGG	TCCGCAGCCC	GCGGGACCTT	CGCCAGCAC	60
ACCGGGGTCA	ACAGCACACC	GGTGGGCTTC	ANGCAGAGCG	CCCGGGTGAT	GGCGGGCAG	120
ACCGSCRAACA	CCTGCGGTAG	CAGTCCGTGC	GACTCCGCGC	TGGCTCGANC	CATGCGCGCG	180
CCGGCTGCGT	CGAACNMGCC	TTGGTGGTTC	ACAGCTTAGC	CAGCANCCCA	ACCGCACTCA	240
GAAACCCACA	CGCGGCGTCC	CCCGGANACC	TGCGCCATCG	KCTGCTGGGG	CGANATCTCC	300
CGATCGCTNA	CANGATGACC	GCTGCGCGAA	CGCGCGCGCT	GCTTCGCGGC	AGCGCGCTGG	360
GCSSGGGCAAC	CGCGAACCCA	NGAACACGGC	AAGCAGTATC	ANGCGAACAG	CAATTGTCTA	420
GGGCTAAACG	CTTACATGCC	AGGATCTCTG	CGCGCGCCCA	CGCTCGGCTC	TGCAGSGCGA	480
CGCGTCCCTN	GGCGGGNCAC	TCTTCAAAGA	TGCGKATONA	CAGKCTAGGT	CTTCCGCGGA	540
TATGSAAGGN	CCCAACCGNT	TAAAGCGGC	SAAAAAATC	TCCCATGCGA	TAAATCAGC	600
CGCGGANCCC	CGCGTSSCM	NGTCVCGHC	ATTNTTCAAC	MGCTTTNACG	GCGGTGCGNG	660
GCCAACTTGC	CAAAWTTAAG	STNGGGGNTT	CGCGCGCGTA	ACCGGCGNTK	NGCGCGTTAA	720
AAAACCGGNC	YTTTCTNGAT	TAMMACCGGN	CGCGCGTGG	CGGCTGKTCC	CANGNTTAA	780
AMCCYCCGSS	MNGGGGTGGS	SAACCTTCC	CGNGGGGTTT	NTGCTTSCYT	AMWCGCGCG	840
AAACCGGKYG	GGKTGGGRTN	WASSAMNCCC	CMGYYTCTT	TAAAGGCCAN	ENRAANGKYT	900
CCTTGGGAAN	CTTNCATATC	GAAATYCTC	CTYMGSSCN	CTYKCRNTN	NRNGGJACS	960
AMWNTYCCNC	GWTTCANTCG	GTCGCGASMN	AAACKCTTTY	TTTTYCGSSC	STCGGGSNC	1020
SGCTYANANAN	AAASATTTMC	TYCNDNANKK	YYCGSSGCTT	CYKMGRRNR	GMGAACCGSR	1080
GG						1082

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTCGGCAC	AGTGATCGCG	CTGAAGCGCG	TAGCGCGGGT	GGCTCGGCTG	GTTCGCGAAC	60
RAAATCGGCT	CGANGTGGTC	TGGTAGGCG	GTGTCCANAA	CGGTGGCGCG	GTGCGCGCG	120
ATCTGATCGG	CGCGGCGGTA	GTGCAGCTCG	CGGSGCTGT	GCAGTCCGAT	GCTCGGAATGC	180
TTGTGTCTGT	GCTTGTACCA	GCCGAAGAAC	CGGTGCGAGT	GCAACCGGCG	CGGCTCGATC	240
GACTCGAACC	GTTCGCGGAA	ATCGGCGCGG	TACTTGAAGG	TCTYGAACTG	GGGCTCAGAC	300
AACGGGTGT	CTTGTGCTG	TGCGGCGGTG	AGTGCGACTT	GCTGACACCG	AAGTCGSCCA	360
NCAACAATGC	CACCGGTTTG	GAACCTCATC	ACAACCGCGG	TCCGCTTOMA	GCTCACTTGT	420
NCGGCGCTAA	TTTNTGCGCC	GGCAAGGCTT	TGCTGAYCAN	KCCGCTCGGC	CAAACTTCC	480
ANTCMSCCA	AGGCGGCGAT	CGNCGCAAAC	ANGTTACGGG	ANAAANATY	CAAGAYCAC	540
CYTCCGGKIN	TTATANTCTC	CCYTTGCTV	GGCGCGCGGN	CYTTGKFNAT	ACCGCTNCCA	600

ANTCCCAACN	CCCXCCAANA	RCYKGGGGCC	CCNCCCAACC	CGGGKGAAGA	WTAATTTAAA	660
CCCYAACMAW	ACTWMMNACC	CNNGGGGCCY	AAMCSTTYNR	AGGTTTTTCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCTX	CCNWTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKGCCCCCY	TCGGCNWNNC	CSGGGGKFKT	KKSTTNCCTT	MMRCNNWYTS	GGCCNASCNN	840
CKYVSSMYCC	CCCCCCCCCM	CTCCGNETCC	CCAMCCYANC	MGGCCCCCTM	GKCCCCWNGT	900
YKCCCCCCCC	AMNNNNNGGG	WGACCCCTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCNGNHA	960
MECYCCNRAR	ANMCCSCNCC	NCCNCRCKNN				990

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTGGGGTG	GCAACGCGGG	CCTGTTCCGC	AACGGCGGCG	CCGTTGGTGC	CGGTGGGGCT	60
GGTGGTGGCG	CGGGCGGGCG	GGGCGGTAA	CGGGGGTGGT	TTGGTCATGG	GGGCGCTGGC	120
GGCGTGGGTG	GTGTANGTGC	GGCGGGGGCC	AACGGTGGTA	CGCCCGGTCA	GGATGGGGCG	180
GCTGGTGTGG	CGGGGTGGGA	CRACNCTCGT	GCCGCTCGTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTGGGCAC	GANGCGSCAA	CGGTGGCAGC	GCGGCGACGT	CNGTTGCCAC	CGGGGGGGCT	60
GGGAACGGCG	GTGCGGGCGG	CGCCGGGGGC	GGGGCGGGGC	TGATCGGCAA	CGGCGGCAAC	120
GGCGCCAGTG	GCGGAATGGG	CGATGCCCCG	GGCGGCGAGG	GCGTCNGCGG	CATCGGTGGG	180
CTGTTGTTGG	GTTTGGACRG	CGCCAACGGC	CGGGCCAGCA	CCAACCCGCT	GCACACCGCG	240
CAGCAGAGGC	GTGGCGGSCA	GTCAACGGCT	CCATCCAGGC	CGTGACGGGG	CGCCCTCGAT	300
CGGCAACGGG	CCAACGGGCG	CCCGGGGAAC	GGGGCCCCCG	GCGGCGACGG	CGGTGGGTGG	360
TTGGCGGGCG	GAAGCAACGG	CGGTTCCGGC	GTCAACRGCG	GGGCGGGGCG	AAATGGCTG	418

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGGGGCACG	ATCCCATACA	GCGCTCGCGG	CAGACCCGCC	CGATACAGCA	60
GCTCGGCACA	CGCGAGGCA	CAATACGGCG	TCTGGCTGTC	CGGCTTGARC	ACCACCGCGT	120
TACCGGGCAC	CAGCGCGGCG	ACCGASTCCG	ACACCTTAAG	CCTCATGGGG	TAGTTCCACG	180
GCGAGATCAC	CCCCACGACG	CCCTTCGGTT	GATAGCACAC	CGTGGTCTTG	CCTATCCGCG	240
GCAGCAGCGG	CTGTGCCTTA	CGGGGCTTCA	GCAGGTCCAC	ACAGACTCGT	GCSTTATAAT	300
TNCGCTTCC	GCGATCAGAT	CGACAATTTC	CTCTTGGCGC	GCCCATCGGG	CCCTGCCCCG	360
CTCGGCTTGC	AGGAAGTCCA	TGAAGAATTC	GCGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
GCAGATGACT	GCAGCTCGCT	CGATWACGGG	ACCTTCGCCA	GTGGGTCTGC	CCCCCGCGAN	480
CTTCGCGAA	TGCGGCTTCC	ACTTCGGCGG	NCCTGCCAAC	GGAATNTAT	CACGGGTTCG	540
CGGTTAAAC	TCTCAATST	NCVGGTCGAA	ATTCGGCAAC	TTCTTATCCC	GGCAGSTRCC	600
AACSAANCAA	ACCTCGGCAA	GGTAGGMITT	TCCCGCNCIT	YCAAAAATNC	GKTTTTTGGN	660
CMRAATTCGC	CKENATGKTG	MCAAGGMITT	CKAANAACCS	GGTCTCTCTN	NTNKGKGA	720
CCAAAMGGGT	TTGGGGMAGC	GDMNCCAAAN	CTWACCCCTG	KTKAANGGWN	TTCCCCCGCG	780
GGGAKKNGA	ATYCYCCSNA	NCCCGGGGGG	GNMCARATTC	TVCGGGMCTC	CTCKGGANTC	840
WNGGTTTTCC	CAAAAAACSC	CCCAATTDM	TTTTTCRCRN	TRTGANACW	CTTTTARCA	900
MMCSAARNHS	ANMCNCTCYC	CKCTKTKTK	AAAAAGNAYN	CCCCMMAATT	TYTAWTTSSC	960
CCSCCGGGN	CCNCNCNTTT	TSCNMTWCTH	WNTNCRMCC	MMMNCKKNSG	KKGGRNCCCN	1020
CCCCNCCCM	AAMWTKSYN	KNTATNAGC				1043

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGGGGAATCG	AGAATCCCGG	AATGGTGAAG	CCTCGGTGCC	TGCCCTTACG	60
CCAAGANTCA	GGGTGAGCGG	CCCCCGGGTG	GGAATGCTGA	GGCCAACCGG	GAAAAGGGTG	120
AGGGCTGGGG	TGGATTAAC	GAAGTTACT	GGGATGGAAA	ACCGGTATT	GATATGTATT	180
GGGCGGATCA	ANGTTGTGGG	AATGGGGGAA	GGCTGAGGGC	GACCTGTTGG	ATTTGGGGAA	240
TTSTYRTGGA	CRKACWGGC	CAGCGGCGGT	GATGGTTTGG	TTSAANTTTT	GTGCCGCCCA	300
CANGGTGATG	GGATTGATTT	TGATGGGGCC	SATCGAAATA	TTGGGTATGC	CNACGCCSAA	360
CGAGATGSCC	GGGACGTICA	TGGGGGGGAC	ABCCMASGGT	CCSANGTAAK	GTTTTCTTTN	420
ATNTTGATCG	GGATTCCGGA	ACTMTSTCGA	TGSGCTCSAY	MTSATSGCCC	NACNCCWCCG	480
YTTATTTCMS	GCTNAYGGGA	ATBAMRGGA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMGGC	540
CCTGWTNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTSTMC	CCSMAAATNA	CCCCCSCTTS	600
NACTCCNCSC	AANTNSCCCC	CCCCCYNNTT	ATSTYCCCGK	GTTCGCCCMC	CCCTTNAAMC	660
TCCCGGTTA	ACCCCCWNT	SNCCNCCCGG	YTAAMNWRG	GCTTSTTNC	CCCCCTTMC	720
CNCCCGCTCK	SAMCNWCCNC	CTCKAACNAC	CCCKCYGSM	TNCCCAATNT	WCMWCKCCNS	780
KTNMTCTKC	CCAAATNRC	CNCRCTCCG	CCXSTSTCAN	WTATAAAACC	WCMYAWYRK	840
KCNWMAWTA	MGACWTCNY	NCCCNCCNCC	NTTKTAMWCC	CCMCCCKCSW	TWCYCKCSCC	900
CCMTCTMNA	YCCGCCCKTY	NKWMCCCTTC	CCCCCTCCG	MCNMBMTCT	YCSGKTWMC	960
NCYNTMTCN	CYNAMCKCK	KCTCTTCGN	CRNTCTCCCG	CCNCCCCCV	KKCTCTSKCC	1020
CNCNCTCCSC	MMKGGC					1043

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

250

- (A) LENGTH: 1016 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	GAGATCATGA	ATAGCGGGCT	GSTCAGCACC	GAAGTGGTCG	GCGATCTCCG	60
GAGCAAGTCT	CGTCTGCTCG	CCCAGCAGGA	GSTCGGCATC	GATCGCGACA	CCTGCGATGT	120
CTTGGATGGT	GTTCAATTGC	AGGTAAGGCC	GAGCGCCBAG	CTTTGCTAGC	AGGGTGTCTT	180
GGCTCTTCGC	ACGTGAGGTA	ACCAATAACT	CCGACBCAGA	CCAACTCCGG	CCCTCGATCC	240
GGGTACGAGG	CTCCGCGGGA	GCCAGCCGTT	GTGCCCCCTG	GSCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAGGAACCG	CGCCATGCCC	GTGCCCCAGT	ACGACTGACC	GAGCAAACGA	360
ACGATCGTCC	TCCCTTCCGT	GGGGGTAATC	GAGCCAGCA	ACCGCAGGAG	CCACCAATCA	420
TTGGGATTCG	GCCACTGACC	GACCAACGCG	CTGTCCGACA	CCCCAGCGGA	ATTGGTGGTC	480
TTCCGCGGGG	CCGCNAACCG	AATCANCGCG	ACGCGCTGCG	CGAASCANCC	GCATANDCCT	540
ACATANCAAC	GGNFTCTGCG	CCACATTTG	GGGTTMTGG	CCCTCNGCAA	CSSNAAYNCC	600
CCCAATTCTG	AACNAAAAAA	TTGGYCCATY	ARNGTCTCTM	CCAAAAACCN	AMTCCCTKTA	660
TCCCCCGGGG	GGRCCTCTY	NNNAAAACCG	CCWAAANCC	CCSGGGGCGC	CGGTTTNTN	720
CCCCCTGCTG	GCCNCGCGG	TTTGGTGMCM	GGSCMTNWN	GGGNTGCSCT	CCNCNAAAA	780
AAAAAYCNG	NCAATYAAA	CCCKYCMAAA	ASKTGGGSSC	CCCMARCCGG	GGKAAKQWNA	840
AMTTANCCN	KAAAAAANW	NCANNMCCCC	NGGNCCTAA	GGKYTTAGGG	GTTSTTNANG	900
AAAAAATMTC	CANATMNSK	TTNNAAAAAA	ASCCSWAKCC	CCCNBNHNNM	CCAAWKAARR	960
SCCTTTCGGG	TWNSSGGGG	KKKKXTNCMS	KMMMTTWGR	CCCNCCGCCN	NFTWRCCTTN	1020
TCCNYGGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGCAC	GAGTCGATTC	GATCGAACCAC	GCCCCGACCT	GCCCCAGCCA	CATGGGCGCG	60
GCCATGGCCA	ACGCTTACTC	GGCCAACTCG	AATCCATTCC	GCCTCTCACC	GCAACCCCCG	120
AAACCGCGCA	CCGCGGCATG	GATCAACCTG	CCCACCCGAG	ATCCGAAATA	GCGTCCACAT	180
AATGAGACAC	TGGCGCAAG	AGCTTGACAG	GCCCGGCACC	ACGCAAGCTG	TTAGACCTGT	240
CGGTCTTCCA	AGAGCGGGT	TGGCCACCCA	AGATACGCCC	GCCCAAGGGC	ATCGACTCAA	300
CGTTCCGCTG	GATCCGCGT	AACGTGCGCG	CCGCCAAGAA	ATGACCGTGC	GCATTACCAT	360
GGCCCTGCTG	ATCAGCTTTG	GCCACTGCGG	CACCANAAGT	ATGANCAGGC	TTATSCCGAG	420
TCTCTGAGAC	ATCGGCAGCC	GCTTCANAAA	CTCCTTTCTG	ACAATSGTAT	TGCTGANCCG	480
CCGAATTCTT	NTCTTGCAA	SAACACTNCA	TCTTNCGGT	NAACAACCTT	GTTTNGAAAA	540
ACANCCATA	TTGAANTCCC	ANTCGGGCCAM	GALCINGTGM	CGGAAGKTGE	TGGGAACGAA	600
TGKTGCCCCA	AAATCCCCCG	NGSTRAAANW	CCCNENATGG	MSAATTTTSC	CTNGAACCAAM	660
AAAAGTCCA	AGKYCAAGG	NGCCCCCCCC	SCNAAATTGG	TGAACSCAKA	WYANKRTCCC	720
WWWTNCAAT	MTTNGGCTCC	KDNTCCCCCT	AAANGGGGSCN	CCCNCCCGGG	GNGTTCCTCC	780
NNNNGGGGMN	CYTCGCTCCA	AAAAAANAN	MTTTCGKXG	SMSEKKCCCC	CCSGGTYWGG	840
GKYYTTAAAC	CCGGGGGGTN	CAAAAAANAN	ACCCCCCAMS	NGGGGGGAAA	ATTTCNAANT	900

AAGGHEKTKC	SCM&CCUCAA	AAANMMNNCN	AMNCCCGMGE	SARGGGGRNY	TTMKAGGEMG	960
GNVCCCCCW	YCGGGGCHNA	NAAYAAAAGK	NGSNGRGAAT	NTNTTTTTGK	RSSSRNETTT	1020
TYNTCCTYCN	CCMNGNRWWG	GRAMNTGKTS	NSSGGGSGGC			1060

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTEGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCCGGGT	GATGCCACAT	CGCTGCGAGG	60
GCAATACGGG	CATGGATGAN	CCGAANGGAN	TCTGGCCTTC	GCTCAACTGG	ATTACGGTTC	120
CCAAGGTGAA	ACGCTTTGCG	CGGAAAGATG	CGACGCTTAA	CTTGCGCTTC	CACCGTGCA	180
TGTTNGTATG	GATGCTGGAA	CCGCTCTGAC	NGATAANGAA	TTGCGCTGTC	GCCGGGCACN	240
ATGGATGCTC	CKSTTTTENC	TCCGCSCTTA	AATTCGCTGT	GCATCATCTG	GCAGGCTATG	300
TTCCCGCTAC	SGTGACAGCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATSCNC	GCGGCAMTTT	CGCAACCTGC	TGTGTNTGAA	GCGTMTCAAC	420
CGAATGCGGC	GCTYAAAAGC	NGGCTTGCGT	TGATTTMMAAC	CMAACCCNTN	CNATYCTTTC	480
CCGNGNMTTG	CTTTCCTTTC	AACTCCGKKG	SYTGCCNCCG	TGAACCCOMA	CTNCCCGGCC	540
GTGGGACTTA	MTNTTCAAA	AAMCGGNTNA	ACCSSAATNN	SAACCTNCCR	TCAAANTAMN	600
SAANTCGGGC	TTYGGENRCC	CCCCNGAAYN	TCCNCCNCGG	GNNNTYCTCN	GCTTYNGGCC	660
SAAACNTTTC	CCRTNCYMMN	TTTACAMGGC	NCTNTMTTGM	GGGSCSNRIAS	GWCCCGGGKE	720
TNTTTCCLAN	TNCNSKTTT	TTKGGGGGGG	GCGYGRTEMC	NCGGGCCGCC	GGCTCKGMAA	780
AAAAANCMISA	RRCCTCYGGG	KKCCCCCCEM	NNATNGGGCG	YKRAAACAA	ACCCCAANEA	840
THONGMGGGC	SMACCSGNGN	CYNAAAKGST	TSNSCTMANM	MXGMARBNCT	SGMSCCMNEN	900
NCTMGGGGKT	TTGNGNGARN	AANAMNGGSM	RCGGNCGENN	GAAAGGGGMS	GSCKSCNEN	960
NGASNGMGW	CHNGGJHRC	NCTGYGMMRN	NGGMMNGNNN	GGGRKNNACN	NMXMCAWSMC	1020
NEHMGNNNS	CGYMTKCCG					1040

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTEGGCAC	GAGACAANGG	CCTGAANTGG	GATCGGGGCC	AGCTGGGGCC	CCTCCTCAGC	60
GACTTCTTGG	CCAAGTCCGG	GCGCCCGGTT	CGGCTTATG	GGGCTAGTT	ATCTGCGGCC	120
AGCTTGAAT	CAGGGCGAGA	TTTGGCGCGT	TTTCTGCGCC	TGGCTTCAGC	TTGCGCGAAG	180
TKGGGAACCG	TCAGGGTTCC	CMAACCAOGA	TGGGATCGT	GCGGTCGGTC	CAGGACTGGT	240
ANTCCTGATA	CTTKGGTACA	TGCTGACCAA	CTGTGNCAG	TATTEGGGCG	GCTCCTCCTC	300
NETCGCGTCC	CGGCGGTAA	GCTCCANCA	TTCTTTTTC	TCGTGCGG		348

(2) INFORMATION FOR SEQ ID NO:314:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCGGCAC	GAGAGACCGG	GTGTTGACC	AACGGACGCT	TGGGCGCGGG	CCCTTTCGCT	50
GGCATCAGCC	CTTCTCCTTC	TTAGCGCCGT	AACGGCTGCG	TGCTGTTTG	CGGTTCTTGA	120
CACCTTCGCT	ATCCAGCGAA	CGCGGATGA	TCTTGTAGCG	CACACCAGGC	AGGTCCTTCA	180
CCCCGCCCGC	GGCACCAGC	ACCATCGAGT	GCTCTTGCG	GTTGTGGCC	TGCGCGGGA	240
TGTACGCCGT	GACCTCGAAC	TGACTCTCA	CTTCACCGCG	GCAACCTTCC	GAAGCGCCGA	300
GTTCGGCTTC	TTGGGAGTGG	TGGCTCGTGC	CG			332

(2) INFORMATION FOR SEQ ID NO:315:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCGGCAC	EAGTCGGTCT	AGACGGATTC	AATGCTCCCG	CGAGCACCTC	GCCACTGCAC	50
ACCCCTCAGC	AAATGTGCT	CAATGTGGTG	AACGAGCCCT	TCCAGACCTT	CACCGGCGGC	120
CCGCTGATCG	GCACCGGCG	CAACGGGACT	CCTGGAACCG	GGCTGAACGC	GGGGCGCGCG	180
GCTGGCTGTT	CGGCACCGGC	GGCAACGGCG	GCTCCGGGGC	GAACGGAACC	AACGGCGGGG	240
ACGTGGGGAC	GCCTCCGGCG	GGATTTCTTC	GCACCGGSGC	ACCGCGGGCG	CCGCGCGCGT	300
CGCACACCGG	CACCGCGGGG	GACCGCGCGC	CGCTNGGGCG	GCTTCTGAT	GGGCTCCGGC	360
GGTNACCGCG	CACGGCGCGC	CCCGGCTCAC	CGCCNGTTGG	GACCGCGGGA	CGCGTNACCC	420
CGATCTTCTT	CCGCMCCCTG	GAAACCGCGG	GGCCGGCCCC	ACATTAKACC	CGCGGNACCC	480
GCGCMCCCGG	CGGAACCGCG	GGYNTTTTCC	AACCGCGGGG	CCGCGGAACC	GMMGGSTGTT	540
CCTTNGGSGA	AGGNCCTAAT	CCCGKCTANC	TYAATCCCGG	ANGGKTGAMC	CTSATGSNCA	600
MYTTMAGGAA	CYTNCCCAAT	KTTSGRACCN	CGCCNGGAAA	ASPAWNGTGT	KGGCAAACNA	660
NNTNCYTTKN	NATTKGNNNA	AAAANCCTTY	CCWCSGRACCT	NCCCCCNGM	GRGMCNNTNN	720
NNTTYGNCNN	CCCGGNNNA	NTTXXATTTT	NGGGGGNTCN	GGSTMMNNNA	AACCCCAAAM	780
MRNNKSCA	ANGGGKNGC	NKNNNNNSGT	TTYCKNNMRA	MRNWTYNNNN	NTCNGASRN	840
NAAMCNRNNE	NGKKNKAA	ARNNTTWKTN	KNSCNNNCNN	GRNGVNGGC	CKMKGNNGG	900
MCNHNANRNG	NNGNCNCKC	NNNNAAAAA	AASGGVNCCKS	NSMKNKCKKG	NRGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:316:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	RAGAAGACCC	CCGAAGGTTT	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
GGGGGAACGC	AACTTCGGCA	AGATCTACCT	TGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTSCGTT	180
GCAGAAGATG	TCCTTCGAGG	TGGCCTGGAG	GATTTTGCAN	GCGACCGCNG	TGACCGCGAC	240
GGGTTTGGTG	TCCGCACTGC	TGCTCACCAC	CCGCGGCACC	GCGTTGACCT	CGACCAGCTG	300
CACCACTCGT	GCGCTCGTG	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGCAGT	GTGTGTGGCG	GCTCCAGAA	GAAGATGATC	GCGAACATCG	CCAGCGCCCG	60
CCAGGCTATG	GTGCGGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGSCCGC	120
CCGACCCAC	ACCAGCTTCT	GTGACCTGCG	TGCTTGCAGC	CAAAGCGTGT	AGACRAACAC	180
ATAAAACGGG	ACGCTGACCA	GGCCGAGCAC	CCCCGCCAGC	AGGTTGCTGG	CGCACCATAG	240
CCAGAAGAAC	GAGATCACTG	TGNACGTCAC	CCGAGTSCCA	ACGCTTTTGG	GCTCGGCACC	300
GCTTCCCGCG	CCAGGGGCGG	GCGGGCGGTT	CGCTTCATCA	CCTTGTGAT	ATCGGCGTGG	360
GCAACCACTT	GAGCTGTGTT	GCGCGGCGCG	CGGCCATCAT	CCCGCCGACN	ANCGTGTGTA	420
GCATGANCAG	CGGATGAATG	GCGCGCGCGC	TGCTGCCGCT	CGTGCCTAAT	TCAACTCCGT	480
CAACAACCTG	CGGCGGCACT	CGAACCGCGG	TGAATGAWTG	AATTAAACC	GSTSAACATY	540
AACTACATAA	CCCTTGGGGG	CTCTTAACCG	GTYTTGAANG	GCTTTTTTGG	TTAAAGGAAG	600
AACVATTTCC	GGATATCTGG	CTTTNTIARC	GAAAAGGCCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCCCTGA	ATGGGAATGG	MNCNCCYKNE	CNGGGNCTTT	AACRCGCGCG	GGTTTTTGT	720
MCCCNCTKA	CNTTMMPTGC	ARNNCGNGCC	SKCCCTTCCN	TNTYCCCTCC	NTCCCCCNST	780
TXCNKKTCC	CNNAMNYTNW	ACGGGGGGCC	VTNGGGKCRM	TWTKTTTTGG	GCCCCMCCCC	840
MAAANASAA	GGGGRNNTY	CTTTGGCNC	CCCAAAAGCG	NYCCCCCCAM	YTNRRNMCY	900
CMNTNKGGRN	CTGTNCKNCG	GAARAMMCC	KCCCGNSTS	STTNGTYWAG	GNNKGNSEK	960
CCSCCCCGGY	MENNAAYAWN	WMMATNCRNS	STNANMAKKN	NNNNNNNSCN	WNGKGNNTCN	1020
SCNSNGGKBC	CSCC					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

AATTGGGCAC	GAGCCGACAT	CCGGGGCCGC	TGGTTGCATG	ACTCGTTGCT	CATCGTCGAC	80
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTC	CTGACCGTGC	TGTCCCGGTT	GGGACCGGTT	120
TCCCGGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGGACAC	ACCTGCGGCT	CGGCGCCAC	160
GACGGGTGCG	CSCGGTGATC	GAGAAGCTCA	AAGGTCATCC	GTTGTTTCGC	CACATCACCT	240
TGCTGCGCAG	TSAGCCCTCG	CGGATCGCCG	CGCTGGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCCGCC	TGAGTGGCC	TCCCGCGAGC	A			311

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTGGGCAC	GAGATGCTCA	CCCTGGGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTACG	80
GCTGATGGCC	CAGAGATGG	ACCAGGTGCT	GCTCATCCCG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGGATC	GCGTCTCTCA	GCTACGCGCA	TRAGCTGGTG	TTCCGCACTA	CCGCTGACTA	160
TGACGCCCGG	TCCGAAATGC	AGCAGCTGGT	CAACGGTATC	GAACTGGGTG	TGGCGCTCT	240
GCTGGCGCTC	ANCGACAATT	CCGTGCTGCT	GTTTACAAGG	ATCGGCTTAA	GCCTTCATCC	300
CGCGCACTCC	CCAGCGCCGC	GCGGCGGGGG	CGGCGCTCTG	TGCGGACCGC	CCGAGCGGCT	360
CAGTGACGCG	ATCTCCCTCG	GCGTTAACCC	CCTGAGAAGG	TGGGTCTGTC	GCAAGTTGGG	420
CCCGGTGACC	ATCNAATCGC	GCGGCGATGA	CGGCTGCTCG	TTCCACACCA	CCTGCGACNC	480
CCCCCAGGAA	CTGGTCCGCG	AMTNCAGGAR	NTTCGTGTGG	GCACCGGCTT	CTTCGCTCT	540
GSEYTAAGCT	TCCNATGTTT	CGCGGGGCTT	CTGGCGTTTC	GNCGGGGCGG	NTCTTTCGAA	600
ATCGGSMMAA	ATCCCGAMMC	AAACCCCGCG	GCTCTTGGGG	GCSSGGGGGG	GGCCNANNCC	660
AAACCCCGCG	NTTAAANTCT	TTCGTCGCGN	CNCGGGCGCC	NCNAAWSCAN	CCCTTTKGGC	720
NCCTCCCGCG	CCCAATTTAA	CCGACGCGCN	AAATCCGAGT	TGCGGCTCTT	KNAAAAAATA	780
AATTGGCSCG	CCCAANTTAA	ATTCCGCGGC	CCCTTGGGGG	CGRANCNYNT	TTTMCSSNES	840
TKGNNAAAMC	NGGAGCCSGG	KAAATMTKTC	NAATCGCGCN	AAMNTTTTTC	TAANNCCGCG	900
YNCCCGGAAA	ATTNNAAAMC	CMGNTGSSNG	GCGGKTTCNC	SGKKGAGGCM	AAAAAANREN	960
EKTNNCCGNN	SAANNCCGNN	SGGNNNNNNN	NNNNCCGNYC	CNNAAAMCCC	CGCGGGGGGG	1020
CCGTC						1026

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTGGGCAC	GAGAAGACGC	CCGAGGTGCT	GCGCTGGGTC	TACAACCTCA	TCAAGCGGCA	80
NGGGGAACGC	AATTCCGCA	AGATCTACCT	TGCTTTCCCG	GAAGCGGCTT	CGATGCGGCA	120
GTACCTGCGC	GCACCGCACG	GCGAGCTGAC	CGAGGATCGG	GCGGCGAAAC	GCTTTCGCTT	160
GCAGAAGATG	TGCTTCGAGG	TGGCTCGGAN	GATTTTGCAN	GCGACCGCGG	TNACCGCGAC	240
GKTTTTEGTC	TCCGACTGCG	TGCTCACCAC	CGCGGCGACC	GCTTTGAGCG	TGACCGGCT	300

GCACCACTCG TGCCGCTCGT GCCG

324

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGGCGC	CGGTGGGCTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTGGCTM	120
ATGCCCCAGG	AGCGGGCCAG	GTGCATGGAG	TGCATGATGA	TGGGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGCG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGGCT	CCAGAGTGGC	CCTGCAMTTC	CNGCGTGCTC	CACGGCAAAAT	GCCTTGATTT	300
CTACTCGCGC	TANTGTTCCC	GCATCGGCTG	CGGGATGAAT	GCGAACCGCA	GGATGCGGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCNAAATCG	GCGCGGACGG	CGCCCACTAT	AANAACGGGC	ACNACAATCG	480
CGCGCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCG	TGNTCGGCG	NACTTTTCTT	NNAWTAAGTG	CCGCTTCGGK	CCCTGGNGCA	600
WTAAATGGGA	AACCTTNGC	CCACCTTGAA	GCGGTTGTTG	NATTTTACT	GSTAACCCCG	660
AATTTTTCGG	GANTCGGTCT	ECGCGGTTTT	YBTNTCCCC	ACCTHGNAN	GGGCGCGCCA	720
AGTTTTTCTT	SYTGAAGGGG	GAAACCCAAE	TYNTTYTYN	AACCSCHNAA	MYMTTYTCGG	780
MNAASCCNKT	CCCTTTTAAC	CAMGGSGGTN	AACCGKTMNG	NGGHTAAAAA	GGGSKHNETG	840
NCCCCYMANG	GGGGGRLAAA	TSTXTCHNCG	GCGCKKAAAN	ACCMGGMYGN	GTGKHKHSS	900
GCSAAATTTT	NMRAACTION	GGGGCCSSEA	NHTTTNAAAG	MSCCCCCNNN	GSTGKCCNNN	960
NTTTCNNAA	WMKKGKFWRM	SNMNSCSNGG	GKTNSSSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGGCGC	CGGTGGGCTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTGGCTM	120
ATGCCCCAGG	AGCGGGCCAG	GTGCATGGAG	TGCATGATGA	TGGGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGCG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGGCT	CCAGAGTGGC	CCTGCAMTTC	CNGCGTGCTC	CACGGCAAAAT	GCCTTGATTT	300
CTACTCGCGC	TANTGTTCCC	GCATCGGCTG	CGGGATGAAT	GCGAACCGCA	GGATGCGGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCNAAATCG	GCGCGGACGG	CGCCCACTAT	AANAACGGGC	ACNACAATCG	480
CGCGCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCG	TGNTCGGCG	NACTTTTCTT	NNAWTAAGTG	CCGCTTCGGK	CCCTGGNGCA	600
WTAAATGGGA	AACCTTNGC	CCACCTTGAA	GCGGTTGTTG	NATTTTACT	GSTAACCCCG	660

AATNTTCCCG	GANTCGGTCN	KCCGGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAACCCCAAC	TTTNTTYYYN	AACCCCMNAA	MYMTTTCGSG	780
MGAASCCNKT	CCCCTTTAAC	CANCGSGGTN	AACCGKTMNG	NGGKTAAGAA	GGGSGNNRTG	840
NCCCCYMANG	GGGGGAAAA	TSTKTCNNCG	GGGCCKAAAN	ACCTTTCYGN	GTGKNNKSS	900
GCSAAATTTT	NMMRAACTEN	GGGGCCSSCA	NNTTINAAG	MSCCCCSNN	GSTGKCCNN	960
NTTTCCNNAA	MMKKGKNNNM	SNMNSCSNGG	GKYNCGGNN	NNAAGMGGGG		1020

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NGNGGGGWN	NTCAYCAYCA	YCAGGGGYW	CAATTGCGGC	CGCANCCTTGT	MAASAGATCT	60
CGAATTCGGC	AMSAGGGAMT	CXCTMGCNCC	GCTGTGCAAN	CCAATRAGGC	CTRATAATTY	120
CCACTCCACA	AAAAACCGTT	GTGTGTATYT	SCCGRAAAT	AAGCGCCCGG	TNTCAACWYC	180
GCCGGTKTTY	CCRATYCCCG	THTTGTAMCT	GCCXGGSTSR	AAAYCCCCCG	TGTTGGAYCC	240
CCGGATTGAA	ACTGCCGGKT	TGAAACTGCC	GKTTTSGCSA	TCCGGKMAT	GAMSTCRCGG	300
ATTAAAAAAC	CGGKKTTSXN	GCTGSGCGTG	CCAAATNCGR	AVCERATAYC	CCATGGCCTG	360
KYCTYCTCCX	YCGGTACCCA	AACTCGGCTA	TCCTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMMTK	TTGCKXGSGT	CCNAATTTAS	CACCASCGET	TCCTTCCATA	CCNAAACNCG	480
CKTGGGCGWC	AGMCCGGAAL	AAAKAATAAT	RAKRAKGGTG	CATNYCCAAA	ACCNCCGCCN	540
CCCNANTNCN	ATCCGNTNCC	MSCNCCCCCA	CCGGTNAAGK	TKSGGAAYTT	CTTMAACCCC	600
CRAANCCCCA	TAACNTNCGR	GAASAAACCC	CTVCNCGGGG	GYCNWNCRAA	ACASCTTTAT	660
TTGCTKSTTT	CGGGMWCGGT	GCCGCCNAAA	YCCCAAASTA	CTTTYTGGGT	CCNAGAKAAA	720
ACCNCGGGCN	CCMCCCSNAA	NWTATYTCTT	KGGCAANCCG	CSAAACCTTE	TOMNACCNCK	780
ATRMTCCCTT	CCCC/SCAAT	TGGYCGGRAT	NCGSCCTTCT	TCAAAXKXSC	CAKWNNGNG	840
GRRNRACOMA	ACCCCAAGTY	CCMMAAAATN	GKCCCTGCTC	CNAACACGNK	TYTTCSSAAA	900
ASCCCNCCCC	CCCCCCCCBA	AACCCCCCNA	RKANTNCCCA	AAAACNYNGK	GGCCCCCCCC	960
CAAACMAAAA	AMCCCCCGSN	RMACSGGGGN	NMCCCCGKXK	KKTTTTCTTT	TKCCMRSCCC	1020
AAMGCAMWSY	KEETNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNVWRSW	CCGSMGMENA	1080
GAASMCCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGGNNN	NATACATCWT	CYGTGYACCG	GGMTCTAKT	GGCGGGCCCG	AATCTNGTCA	60
ASAGATCTCT	NAMTTCGGGC	ACAAAAACTW	GACAAASYMT	CGNGCNMTCC	GTGTCCCTNA	120
TGCGAAAAAG	NGTRACASAC	ASACACRTAT	GTGTGCCAC	CASCAAYTCK	TTGGGACCTC	180
GCTEACCGGY	TGCCCRNACG	CCAGGYTGCS	CWCTATCCC	RACGCCGCC	ACGGGYGGGG	240

ATATTCACAGG	CACCACGGCC	AGTTTGCTGG	ACAATGCCCT	GGCAATTTCC	TCRAANTTCC	300
TGAAACCGAA	TTGNTTGA	ACCCGCAAG	CCCCGNCNR	AACATTTGGG	WTCCGCGGTT	360
CTCCCCACCG	KTTTCGCGG	GTNTGGGCA	AAGCCACCC	WTGGWTTCTM	TCNCCGACC	420
GGGCGGACAA	NTCGGTTGC	AATTTTGCA	AYCGGGGCGG	GGATTCSCA	AACGGGTGCC	480
GAAACTGTTY	YCAAMACCG	GGAKCGCAA	TTTCGGGCR	ANAAATTTCN	YCNCACACT	540
GCTTCTACTT	CCCCGACCGT	AACMANTTTC	ATCCTCTNN	CCTCTGCGCT	TGGGGCGAGG	600
CAAAAVACCG	CMTTGGGTTT	CGCAACCTGC	GGCCCAANTC	CCNAMCCCA	CTTTCTATTT	660
GGNTCGAATT	SCCCCCCGGT	RAAAACCCCC	NTGGCCNNYT	CGGASSAAA	NUGGGCCCTNT	720
KGGCNSCCCC	AGTAANACCC	TACCNNAVTS	CANTCTTTGC	CAAATTTGGG	ACGAANSKTC	780
GGNTCCGGR	ATTTTYTTGS	GGNCNCCCTN	TATNGGSENTN	GGGCCCTCNC	NCSTKTKGCA	840
NASSKAYCCS	NGNKGCGGGT	ACCCCGCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTC	900
GCCCCCMNGG	GGAAKAAATWT	MWWTMCNSGG	GGGAANTTTT	NTSTGGAMCS	SGGACTCCCR	960
GGGGGNTTTT	TCCCCCNCSA	NNANANGGGG	GGGGGANAYT	NTGNSGNGGG	KWNTTTTATTT	1020
VTYTCYCTM	TKACMSGGGG	GTTTCKAKNS	GGGGGAGAAA	ANAAAAAAA	RAKGGTYKNTT	1080
TSKNCACNCT	GKNWNNWANN	NAGAGKTCTT	CKCKCCNCSS	SNFTTCTTTT	MGNSSGYGGG	1140
GNNGNNNRAA	ACNRSHMAC	KCSYTYCCCG	CGYTCTCTCC	NENGGGGYGS	NGSCSNSTYN	1200
GSHKGRKNTA	TNTMNCCTN	SCCTCCNCCC	GCNNTTCTC	TMTCMYGGG	C	1251

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAYTCGGCAC	MUAGTATCAC	CAAKCTGYTT	GGCCCAGCAA	AGTGGAGCTA	TTACTACCTG	60
TATGTGATCC	TCRACATCTY	CTCCGCTAC	KTGCTCGGGT	GGATGGTGGC	CTCGCKTBAE	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAACCCCTTG	CGCCCAGCAC	ATCAKCCSCG	180
AACAGCTGAC	CTGCMGCCCC	ACCGGGGGYC	GNCAATAACT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNAC	CGGTGTCCCA	ANTCGAACTC	ASCCSSCNMA	CCMMAACKA	NAACCTTGT	300
CTGAAGCCCA	GTTCAAAAAC	CTCAAGTWCC	GGCCCRACCT	CCCGAAACCG	TNCGAGTCKA	360
TCRSAGSSGG	CGGGGTGCMC	TGCAACCGGT	TCTTCGGNTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGNTC	CGMGTGCCCC	CGCCGCAAS	TTTCTACCG	GCSSGCCNAT	CRAATTGCGC	480
GGGAACSGSN	CCNCKXTCK	GGAMACGCCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCKGY	540
NAACNCCCGA	NCNCCCKSKT	TCGGGGCTTC	NMSGCGAATA	CCCKNSCMT	CGAATCCAA	600
TTCCCKMYGS	CTTTTYTYCC	CCCCGGCCCC	AAAYNGGGYC	CCTASSNMKC	KNCCAMNANT	660
CCNWTCTGSG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMNA	NMNRGGGTPT	TSCYACOMMN	720
AACCGKNNES	KCCCCMKCTK	MANAAAKATT	RATCAMKWN	GENCKCKMCH	NAAMACCSCN	780
CNCYNCWYTC	THYCSSKNGC	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMT	CTMTCTCNET	840
MGCGCCNNTN	TYCKSGAKAT	ACASMNKTC	GSCNCGCCCN	MAAMANRAJA	CTAKCCGYGN	900
CCNSNTMTN	CTSNMMNBN	TCCWNNATC	NTTYGKNCN	KETMKATNWC	CSCTSECNCK	960
MRAMTKTYG	SNCTCTCTCA	TONTCTCKSC	SNMSKNTCK	KSCNCCNWN	CNKCNMKCN	1020
GGNSTCCTCY	TCTGNTCTCS	AGCKCSENC	NACNCACACK	NGWCTYTTCC	WTGNMKCNKM	1080
TCKCKCACRS	MTMTCWCCS					1099

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid

258

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GNGNTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCGGCGG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MSAGCGGCAC	AKAKYSTCGT	COMRACCCGG	CAYACWCCWS	CNCSCCCCTT	120
CTTRGACCGG	GGCKATASMC	ACCGTTGGCC	CGCGCNCSCA	CCTACACCCAC	CCACGCGCGC	180
AGCGCCCCCW	TRAMCAAAAC	ACCGCGCKTT	TACCGCCCGC	SCCGSCGSGG	CCACCACCAAG	240
CCCCACCGGC	ACCACCGGCG	CGCGCGTTGC	CAAAACAGGC	CGCKTTTTGC	CACCRA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNLSGNHMY	ATCATCTTTC	TGCACCGNGG	MTCAWTTGCG	GCCGCAATCT	TSTWNASAGA	60
TCTCGAAYTC	EGCANGARCA	TCTGCGGGGN	GAATGTCCAA	AWGTGWKTAA	CGGCMATCGG	120
TTTGCCGYCA	ACCACCTRT	SCAKATGGGG	GCCAMWTYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTCG	CKTGTRASCA	ACCTGCAGCG	GCTCAASCAA	CAGCTCTTRA	ACCGTAAATY	240
CKTAGGTHET	YCCGGCAACA	ASCYCRATAA	TSCGSCCGCG	AMCCLACAAA	CCTGRNTNGT	300
TNTTCNCRAA	NCCGCTYCCC	GRAGGGGTGA	ACTGCSGTAR	GCTTNTCNYC	NCCCTRACAT	360
TAAACCCCGC	CGGNTCTWCG	CGCGCGCCAA	ATYCTTSCCG	WTGCGNACCA	YCCCANCCTG	420
CGGTATGGTG	RAANCASTGG	GCRAACGGTM	MCCGTACCKC	TGGCTGATYC	KTCCGNTCCS	480
SNAAFTCSGG	GATTTACCGG	CAMGGTTAAY	CCAGGYCCCC	TNTGCTYCKY	CNACLAACCG	540
ATCMWNCNCG	TACCTKTYAA	AATTCTTTGT	GCTGGAACCG	ANYCKAAAAA	NMTNTTYCCN	600
TCCAMMSGGG	CYCGGAANKY	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNCGCC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCTTCN	TGCCCCCTTA	AATTEGNTYC	720
AATCCCKCAA	CGCTCCCGCG	GGTCCSCCMT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSG	780
GCHGTMAATW	CNCCCNNTT	CYYGKNAAAC	SCCCCCWKEN	GCCTYCCCN	SNTTSSGCCS	840
GCTTSGAMYC	AAAANTNGGG	MMCNRAAGNC	SGNAMCCSCN	GKKGGSATW	TKAAYCYVGG	900
GGGGGTCHYC	CCCCRCNAA	AAGYGTGGCC	KCCSSSCCTC	CCMARTTTYT	CNGGMSCHAM	960
ACCANGGGNG	CTCCCCNCG	WGGCTCCCN	SNSMAMAAAN	NKCKCCXGGS	CKGAERNMNA	1020
MCTCSNGNGG	WTCCCKNRTC	NSCNGNCGG	YGENSASWCC	YNYCNCACCA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCGTTT	TTTATTTCAV	TCATTCACCG	GGMTCTAGTG	CGCCCCGCAK	CTTGTCKACA	60
GATCTCGAAY	TCGGCANGAS	ACAATSTCGG	GTKGGGCAAT	GTGNGGTGGG	GCAACTTTGG	120
GCTCGGRAAT	YCGGGGTTAA	CGCGGGGTCT	RATGGGTSTG	GGTARTATCG	GCTTTGGTAA	180
TGCCGGCASC	TACAATTTCC	GTTTGCCAAA	ATATGGGTGT	GGCAATATN	GGTYCGCTA	240
ACACCGSCAS	TGGRAATTYC	GGTATTSGGT	NACCGGTRAY	AAVCTGACCG	GGTNCGGTGG	300
TTYCRATACC	GOTAACGGGA	ATGTSGGTTS	YYYACYCCGS	GSAACGGNWW	YTTNGKTCCT	360
TYMCNCTSSM	CKSAAMTSM	KMGSTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CCOWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	SGSGVCTCA	MNCCACTYTG	NGYYCCCTCC	MMCTCYCAYT	480
CMSTCCGGTW	CCTNMMNCC	CSCHRYCTC	AMCNCTESGE	CACCNATMYC	CSACKCTCT	540
MCYMCSCAKN	MTCCCTCTCN	CCTYTNCCCA	MCNCSCTCTM	TGMAACTCEK	CCGGYCKCNC	600
MYCTCTCKCC	AYNMAACCKK	TYCYWCHWYC	YMYCKCKCAG	WYNNMCTCCW	ACTCTMNTT	660
TCTCTCNKCC	CMKACKNTT	CTCNCSCCCC	CCACAKAYMC	YAWCMTMTCC	MCTCKACSCC	720
CYYCBFYCCM	NMCWCMTCWC	TWNACANCN	TYCTCTCTCT	MMMTMACCKC	WCHSTCNCKK	780
SGACCTTCTC	ACTEMKCCCK	TCTCTTMCX	CCYMWCTTCC	MKYNCCCTCC	NMTCTMCKYT	840
CCTCNCMRY	CYYAKCAKC	NMCTCCCCAN	KMCACCTECT	CCCCCAKMS	ACNCKCCCCW	900
CCTCCTATCC	WCTCTCCTY	ATCTCCTCN	CNYCYMYMCM	ACNCKCYAYT	CHACTMNMGN	960
CCANCNCTCT	CTNYCTCNCX	ACCTYCKCKK	CTMCKCNYMC	NRNCTYRCCT	CKKCCNCCRN	1020
CKNMCNCKTM	CTCTCCMNM	TCCCNCCCAT	CTMCKSTCTC	WNCNMTCCCT	CNKCTNYNT	1080
KCTTYCCMYG	CTTCNCTCM	MCCNCCYATC	TCTMCKCTCT	CNCACYMCAC	NNTTACNCKC	1140
ACTCTCTRCW	CKCKCKMCCB	MTCTCB				1166

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

NONNNNNNT	CWTACATCMN	TCTNCACCSG	NGMTCWATFG	CGCGCCGCCW	NCTTGTMMAS	60
AGAATCTCMN	AAVTCGGCAC	ANATGTCTTT	TSTMTAKTGT	GGCGGGGNGC	CACGCCNTAT	120
GTGYGCTCTG	GYTRACCCRA	CCCCGCGGCS	CGGGCCRACC	AGCGGGGGR	TSCAGGCCSC	180
GGCGGCCGCG	GGGYTATAT	BAAGCGCCGY	TTTCTRATA	ACGGTSCCSC	CGCGGGGTRA	240
TTACGGGCAA	AAVCGKXKT	TTGGGTREAT	AACGCTAATT	GCAACCAWTT	TTTYCGGCTC	300
AAAAACTYCG	CGWGCANATC	NCGGGYCMCT	RAGGCGCAAT	YMGSCCAAAA	WTNTGGGSCC	360
AAAACCCCKT	TSYTATTTTN	TGGGCTATSC	GGYTGTCTCG	GCAACGCTY	CCCGGTTAA	420
TCCCTCTCGC	GGCGCCGCCN	AAAAACEACC	AATYCCGYTG	GGGCTGKYCC	CMCAGGCSGT	480
TGCTYCGNGY	CACCTGGCCA	AAVYCCCAWT	AKATTEGGTG	SCYCKTSCGG	TTSYTGGGCT	540
CAATTACCCC	CNCGGNAAL	GRRAAANAA	ATCNTCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGGG	ATGGCSGGGT	TYTTTACCT	CAAYCCCCNA	NCANTWACCT	YTCCSCCCCG	660
GGGNCANAA	CGSTNGCTC	CGSGGNKCC	TGSTMCCGN	ATCNAAAGGC	CNGAATTTGG	720
TYSSSTYCHA	ATTWTKKXY	CCCCWCNTTG	YAAAAAKCCA	AAASAKCCCK	YCNCAMMYET	780
NGGGGTYSEG	GCCGTYCTTK	SNMTTAAACC	CYCCCCAAAA	YVNSGGGKKT	TCCGCTNSAT	840
KCCACCNCCX	GNGGGGGGNA	SAAAAAAAY	TTTTYCCSAAA	ATCCCACTTY	TCYETESTRY	900
ANACCCCTTT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCCCCK	960
CSGGNGCCCC	AAWTTTGKTY	YNCNANTTYC	CCCNAAAMCM	AWTMGGGGGS	KCCATTCTGG	1020
SCYTMANTA	AAANAANGGG	SKTTTTYCTY	MANAACAACN	GTGKCNMCMN	CNAAMAAASN	1080
AKMAAAKAGN	KKMTYKNSA	AANCCNCCCC	CTSTYTNYYT	NETNMCKCC	CYGGKCKMGM	1140
SWSWTNTTCT	NCCCRCCCC	YDYNKTGANA	AAMNCCYCCS	GGSTMCRNAN	ASNMTTTCCK	1200
STSTNGMGCC	KMBASNANAN	MCAMWXYCC				1230

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

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MNGGGGKNNNA  THAYCWTCTC  ACSSGGTCTA  TCCGGGCGCAW  CTMGTTMAASA  GATCTCNAAY      60
TCGGGAMNAN  GGAIMPDMKC  CATATATAAC  CATTCGCTCS  GYWTGCAWCT  CRAAWCTGTC     120
CTTCSKGCCG  TTKTACRAAG  GTGGMWTGYT  CWTYCCTRAA  SCCCTCRATC  TCKTKTATYC     180
CTKGGGCTYC  ACTTTAACGG  RATXSTGCC  TTKTAYCAAT  RATGCAAWTA  WTGGYCAAWT     240
KTTGCAGGCC  RACGGCWYCT  TTTYCCGCA  GRACATINGA  TTGGANYCCG  TYCCCRAGGC     300
CCGGCAGCAR  ACCGGGCMCC  AAAGSYCCGC  GCRAWTSCTT  GGETCRAAAA  TGGTGCMAAC     360
AAAMCNATCC  CCGGYTTRAC  CCGAGTTAMC  ACAAKRAAAT  TCCGWTGGCC  GCACCAWNTT     420
TTYCRATCWY  CWYCCGCACC  TTRAACCTTK  YTCCSGTATT  GCCTKCCCTG  CTCCACAGCM     480
YCNCCCKTCA  AACCTGCGGT  GACTCCAACT  GGTCTGGYCG  AASGGGGGYT  CAMCGGACAA     540
AACCCCRANN  TCGCCAAATT  TCCNCCCCC  CYCGGGAAN  GKTSATMTTC  TCSNAACCSA     600
CMGGGNNYTW  NAACCCGTGA  CSSSGSNKGA  MYNSCCSGGA  ANTTTTCCCT  TYNGGGCGRN     660
AAANCCCTTT  AAGGTACCC  KGNNGGGGG  CCGYTTGGG  AAAACAACCC  CKATTGGKTT     720
TGGAAATWTT  TCCNCCCCC  TTGNSGGGG  GGGCCCCAMC  CCMCTTTTN  TCMSCNMTYY     780
YCYGGGAAT  TNYTCGCCG  GAAYYCGGM  CCGYCCCTAA  NCCCCMHWGG  GXYSTGSNAR     840
GGRATMAWNT  TYSTTTTYMC  CCGGCMNCCC  CCGAKMCT  KGMTGAACMA  AAACCSGGGG     900
GSCNMYMWY  YCNMKNRIT  TNRGSSSMT  TYMAAAMMAN  GGGGKYNTTY  CECNCSGN     960
GKTVSGGGS  TTTCCTTTT  GGGSATYK  MACCCCKTMT  AYCCGGGGST  WTKTKYCCCC    1020
SC                                                    1022

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

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MNCGRNKNFTA  TAMAYCWYCT  NCACCSGGGA  TCWATTSGGG  CCGCAATCTT  STMAASAGAT      60
CTCKAAYTCG  GCAMGANCEG  CAWCTATTTG  KGTGRASCSC  ACCAGCGRGA  CCTCCCSGXT     120
CKTTYCTTGC  AGRGAGGCC  TGGGTGGCRC  CGGTGGCAAT  GCCAACCGGC  CCCCRAAACN     180
CCGCAATWY  CRAAAAACAA  CCGSGGGGTA  GKTCCSGGCC  GCCAAATMAA  TAACCGTETT     240
AACKZAGGCN  ACEGCEACCC  GGYCCCCGCC  AACCAAGCNA  CCTCCCCSCC  NATAGSYCCG     300
GTGGGGGCTG  CCKTATYKCC  AASTCCTCAY  CTENACGGGM  CGGYCCMCWT  TCCGCTCAT     360
CGGTCTCTGC  TIMMATTTC  CRTCCACYKS  GCGGGGAACY  TTTTNTYCN  COTTGSCMAN     420
CACCNAAAGY  CNAAAATTNC  CCKTCCCKYG  SNNCAAAYGR  GATTGGGGTY  CGKXTTTTNT     480
TCNMCCMAAC  CCGCTTTTNA  CCCCCCMATC  CCTWATACC  CCGWMMCMNS  ANGKTTGNSA     540
AAKTNNCCCC  AATTCCEAAA  MTTCCTCGCC  NTTMTWMCY  VYCCTTTCCC  CMCCCNMAAA     600
GGSCRCCTTY  TCGGGAANTY  TCCCNCRAA  ANTCAMNCCN  TTTCCNCCA  AGAANTTCGG     660

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261

SACTCCTTTT	TTTNGGGNAM	ATANATYTTT	YCKTNGGGGSK	TTCCGNTCNC	AMMAATNTCC	720
EGGGKAAMCC	AGKFTNTTCC	YTTYCCCCAA	NNTYCCYKGG	RMCYNNYYCY	TTAAANZASR	780
SAACCCCKGG	GKCYNCNCSS	TARCCCCCAM	KAAAATTTCC	CCCSSETTTC	TYNNKCKMRN	840
GCCTCCSAAM	ACTMTWAYTT	TCCCKCGNNN	TTTSYCCCKCS	KCAMWMMMTG	KIMCTTTTTT	900
YCSMATAMA	CTTNGGKCC	NTCNVGSQCS	CHAAANAAGS	CSCGSTTCTN	TTCMNMACA	960
YNTSGNMMA	SAAKAKWATA	ANNNTREKYE	TKNNCCCNCC	CKCKCTTENN	TNCKCKCSKS	1020
GGGKNNKKR	GWCTCCWENC	CKCCNCCKNK	CKKWATMCCC	CCCCSKCCGM	NOMBNTTNTT	1080
CCC						1083

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT	MCAYCWTCTG	YACSGGGMMK	TATTGCGGCC	GCWYTNNTM	GASAGATCTC	60
GAATTCGGCA	MGAAAAAAGN	GATGTGCTGG	ACCTTMCGGC	GCGGGACGCR	ACCRACAAAG	120
RAASGCGCGT	ANAATATTGG	CCACAKTTGG	TCACATATTT	ACCCAATTMT	AYCAGGGAYT	180
MGCAATTCGG	GGACCRACCT	CACAACTCCC	ATSTGTGGTT	GCRACCCCTR	ACCGTCCCCA	240
MYTYCGCCRA	STTGAACCCAG	GGCRAAAAAA	CGGCGGCCCC	CTCGCCCTGA	NTCCCGCTCS	300
GCSCNAATAA	CTAGGCCCCAT	TEAACCGAAC	CGGCGGCCCC	NANTTGGCCA	ACAGGTCCCT	360
ACRAAGGGGC	CCCAHYCCGG	CGGWTCCCGN	TTYCACNCCC	TNKTCTCKTG	CCGAATYCGG	420
WTCCRATNYC	CCWTGGGCGT	TETCKYCKYC	KYCGGTNCCA	AWTCTNGGTA	TNCTATRGKG	480
TCCCTTAAT	SCANATCTGG	GCKYCCATT	NCTGGGNTTC	NATTTAMMAN	SRRCGGTTCT	540
TTCTTTCCRA	AACCGSNTGG	GGCCNMMCCA	AAAAATGATH	ATAATAATGX	YGSCTTTCAA	600
ACCCCGCCCC	CCGATTCRNT	CGGTTCGANC	CCCGNGGGT	TAAGKTGGGA	ATTTYTNAMC	660
YCNASGCCCT	NATTTGGGNA	AAACCTTCYC	GGGYTCGAAA	CMNYTTTTTT	GSKSNTCCG	720
GCCTCTTSSC	CAAAACCCAA	ATTNTGNYGG	GGYCCCTNAA	ACMCGGYCXC	RCCGGAAATT	780
TTTTYGGTTC	AACCCCAACC	TTTTCAASCC	NTTTTTTYTT	TGCCSSCSMN	TNGSSGGGNT	840
KSSCENTTCT	BAKELCCNNN	GGGGGNYCYM	CCCCCMNTTT	CTTTTTTTTT	CCGTNNMAAM	900
NKKTCTCTCA	AASMCCTCCC	SCCCGMSAA	ACCCCTTNAS	GTTTTTYCHMA	AASWYDRNGN	960
KNCCCCCCCC	MMNAAAAAAY	YCSCCDNRN	ACSMNGGGGA	MCCCCCGGSN	NTTKTTTTTT	1020
TNCSGTYCCC	CSRMASYTTT	TKANAMAMNR	GAMNSMTTTY	TNNRCNNNK		1069

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NGNNGGGGKWE	MATACATCMT	TCTTCACBSO	GGATCWATTC	CGGGCCGCM	TCTNNTMCAA	60
SAGATCTCGA	TTTCGGGCM	NACCCACCCN	TCCRAAAAAA	ACCCRAANCT	CGGSKCTYC	120
GAAAGTGT	GCCCCCTTTE	AATTTAACAA	ATTCASTGTC	ANAGTGTCAC	GGCTTACWT	180

262

YCCGGGCAAA	GGGGCCACAA	CCTGCAGGGA	SCACYCRAAG	GRTGYTGRTS	CNCGGGCGGG	240
CCGGKTNAAG	GGACCTGCCT	GGGTXTGESC	TMCAAAATATC	WYCCGGGGGT	YCGCTGGHAT	300
MCNCAGGGGT	GTCAAAAAC	CGCAACAGG	CACGCCANCC	NTTTACGGGS	CTTAAAANGA	360
AAAAGGGCTG	ATGCCCCCAA	GGGGGCGCGC	NCCCAACCTT	CCGTGGGTCA	ACRACCCGGT	420
CTCTCKTSCC	BAATCCGHW	CCRATNYCNC	CWTGGCCTTK	TCKYCTYCTY	CGGTACCCCA	480
ATCTGGGTAT	CCTATASTGT	CCCTAAWTT	CCAAATCTGG	GCTGTCCATT	TSCTTGGCNT	540
TCCAAATTTA	CCANCAACGG	TTTCTTNCAT	NCCAAAAACC	GNTKGGCKCC	NRACCCRAAA	600
AAATGAATAA	TAATAANNGG	KCNNTTYCNA	ACCNCCCCCC	CCCNATTCCA	TYSNSTTCCA	660
NMNCCCCCAG	NGGKTAGGTX	GGGAAANYYC	TCMACCTTCA	ANCCCTWARS	TTTTNGRAAT	720
KAAACCCCTC	YONGGGTCWW	TYMRAAAMA	NTTATTTGGH	NGNTTTCGGG	MWNCERKIST	780
SCCAAAATCC	MAAATANTTT	YTTGGTYCNA	TWAAAAAMCG	YGNCCMNCOC	GGAAAAATTT	840
TTTTGKTTSA	ACCCCAAAAC	YTTTTCMNAA	NCSSKTTTTY	CYTTCCCCCC	AMNWTGGGYS	900
GGGNATGTYG	SCYTTNTCTA	TKTKYTYMTW	CMGGGGGGNN	MMNTCMNCCC	CCMTTTTYCT	960
NYWETTTTIN	KCCCCKTMR	NHRAANNGGN	YTCYNANAA	AAGCNCCCCC	SCCKNCCENA	1020
AAAAHCCCCN	NNNARAKTNT	TTMEANRNMN	SKCKNKWKY	YCCCCCCCWC	YNMNNAAAAA	1080
AATMYCCNCC	RASANMCASM	NMGGRGNRSC	CCCCCCCCST	NNNNNTMTNT	TTTTTTCSSA	1140
GAGCKCCSCG	MSHANMKXCK	CTTTTTKCNK	NNGRNGNGNN	GGNGMNCCKC	CCNAGAAWVK	1200
CTKSTCCCKE						1210

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSSNONNA	TMCACTWYCT	GYACSGGGMT	CWATTCGGGC	CGCAACTNGT	MAASAGATCT	60
CGAAYTCGGC	AAKAMACACT	ACCGCGGTGT	MTATACACCG	CAAAATGTTCT	GTXTGCCAAA	120
ACCGAGACGC	GCGGGCGGGG	GGGYTCCAAC	GCKTTACYTR	ACCCGCCAGY	TCAGTGTTRA	180
AACCGGTGYT	EAGGGCCSCA	CCCAACWTAA	ACGCTTTAKC	CAAGRAWYTG	GKTGGCCCGC	240
AGCCACCTGY	TGTGGYTGCC	CTCWYCGGTG	GTAGCGCCGG	TTANCGCCGG	TTGCGGTYTC	300
AMCASCSCGC	CGGTRATCCC	AKCNWTCGCC	CGGCCMRACC	CACCGGGCAC	TTTGRACGGT	360
GCCGCCAATT	CAAYCKYCT	GRWTCCTTCA	AAACACCAER	AAGGCCACCH	CCMSCACCHN	420
ATMGGGRACT	TTAAGSCCCR	GGCAAAACCT	NTRAKCNCT	CCCGGGCRAA	GGTCCSGCAA	480
SCRATCCMAA	AAAKCKHAT	TTCCCCCAGC	AKCAACCCAA	NMCGSTTTGC	TGCTTCCGGA	540
TTCCGAAMCCA	ATTMCWGGKT	NONWGGGAAA	AACASCNNCC	NWTAKCCMGG	CCCMCGGGCA	600
ATTTCSGRAA	SAACCCCTNY	CCCGGTTTTT	YCCTGCTCMG	GCCCAANACC	CCCGSGAATC	660
AAAAASGGTC	GGNCAANNGG	GCMAAACCCS	SACCCMACTT	WTTCCRCCTN	GGGGSGSCWN	720
CCXNGTTTAA	ANKSCCTCYT	CTSCCCAAAY	TCGGKCMAAA	NNRKTGTGGK	TYNGGCMACC	780
NTTTCGGGKC	CGGGGCKKSE	WGYCTMSMA	CTTTTNTTTT	SCCCCYKRAA	NYSCCCCCCC	840
CGSSSCCCCG	CCCGGGGGGA	NNTTTTTAMA	GKITYCCCCT	CCCCAMAAA	ANACCCNYC	900
CCSGGSCCCT	TTKRWAAAMN	KCTSCCCCNK	GNNGGGGCKM	GKTTATTMT	NNNCCSCCCC	960
TCCCGGSAAA	AAATAKNTTT	SYCCCCCNC	CTCKKCKXNR	GKAMSMSCCG	TCCCTCNC	1020
GCKNTWLAN	ARSNCCXNN	CCNCKKCCG	NSNGKCNWCD	NCCSTENCT	NKGCNCKNEN	1080
KAAANAAYNC	NGSMSTSSMN	CNKCC				1100

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs

263

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGENENNNNN	TAMAYCWYYC	TSCACSNNGA	ACWANTGCGG	CCRMAMCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCCGC	AAGASTGTGT	GCATCTGGTC	ANAGTSTTMA	CRCGGTGCCG	120
CSGGTGGKTR	GASCACMCAT	NTGCGRACAC	CAAACCCCTC	GCGGGYCACC	GGCKTGGCCT	180
GCAAAWYCCT	CCAGGCCACC	TCRAACAAYW	YCTYCTGCAA	CGCARGCCGT	TYCSCGSCCG	240
RATCCTGGGT	CASYTCGCTE	TGCGGTGCCC	AAGTACTGG	CSRAYCAAAA	CCGCTCCGGG	300
RAACRAACEY	AAWYTGCCG	AATTTCTTTC	CCCTGCGCCT	TCATAAATTT	NTNAAGCCAC	360
CGCAAMECTY	CGGGCKTCTC	CTCKTGCCRA	ATYCGRWTC	RATAYCGCCA	TGGCTTNKTC	420
KYCTYCKYCS	GTACCCAAAT	CTTGGGTATC	CTATANTKYC	CCNAAANRCA	ANTCTGGGCK	480
KTCCATKTS	TGGSKTCRA	ATTTAMPACA	NCGGTTTCTT	TCWTACCAAA	AACCSNTGGG	540
CCCCRACERA	AAAAGATAA	TAATAAGGTG	CMWCCAAAC	CCCGCCCCCC	ERTTCARYCS	600
GTCCARCAAC	CCANGNGGYN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	ENTTNSGNAA	660
AAACCCCCCN	GGGYMYCAAA	AMCCTTTTTG	GGNMTCSGS	CCATGKYKCC	AAAACCAAAA	720
TWTTTCYGGT	CRWAAAAACC	GGCCCNCCCG	NAAATTTTTT	GCACAACCCA	AACCTTTMMM	780
CCNNWTTCTY	YCCNNAACAA	TNGGSGGNGN	NGSSCNTTYT	TWTTTTYMAA	GGGGGGERNC	840
SNCCCCNAAN	YYCNAANKG	NKCCCGSNMA	AAAGAGANTT	YCMKAAAAAC	CCCCCNCCCC	900
NAAAYACCCC	MAAAKWTTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NRNNGNNNNY	ATMMAYTCWY	YCTSCACCCG	GGNNWCMATT	GGGGCCRMAN	KCTTGTMAAS	60
AGATCTMMAA	VTGGGCACAG	ASSSGCACAG	ASCCGCGGCG	CTATYCMYCC	GYTGTCTCATG	120
CTCAACACCG	TCTTCGGGWN	GRATAATGGC	NGCCGCGCGG	CGCCAACACG	YTCAAYTGCT	180
TGCCCCAAGC	CATATNTCAA	CAAGSTRATA	AAASCALAAC	CGCSGCGCGY	GGCCTTGGGC	240
SCGGRAASCG	GTGCCAACCC	RAACNCCTT	GGGCACYCGG	KTBRACCTTA	AAGGTAATC	300
TCKTCTCTCT	GGGCTATGGT	GCGCCACAAA	CCTEYTGCGG	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRCTTTT	TATWNTCEK	YCTACACNCT	TGGGTYCAAC	CAACCCACTT	CACMAAATTG	420
TTTTGGGKTS	GGSSGCGCGG	YGTNNCCGK	TAATAATCSG	NTGKTCGGCC	MYCACCGGWA	480
CCATANGCTG	GCCGCGCCTG	GCAAAATTC	SAAATCATYT	CGTTCTGRAC	CCCCACMRC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKINCCCVAA	TSCAATTGGG	TTYCCNTTSC	YGSTTCCAA	TBRACAAMAS	GGTTTCTMT	660
ACCAAAACCC	NTGGSCCINA	CMNAAAANA	RAAAANAKGG	KCTTTTAAAC	CCCCCCTTAT	720
TCAWYGGGTN	CNENWCCCGG	NGKAAGGKGN	GAAAYTTTRA	CCCAANCCMT	ABSTTSGNAX	780
AAACCCYCYG	GGGTSMCAAA	MIGNTWTSSC	CTTCGGMCTT	YCCAAATMSA	AAATTYTCEK	840
KRMNAAAAMC	YGNCCCCSAA	ANATTTTTGT	NAAMCCCIQA	YTTTNTMCC	WTTTTCCYCC	900
CCMKNNSNG	GNINCCCTTY	TIATTTCTNM	NCNNNSGACN	CCCCNTTYTT	TWTTCKCWCH	960
MMARGSNNTT	RGRMMNNCC	CCNCCCCNAK	NTCCNCAAAK	NTTTNAACMN	NNKYCKCCCC	1020
CCCMWNNKIC	CCCMNCTMT	TM				1042

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

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NNSSGSMKKK ATAMATWCT CTSYACCSNG GNTCWATTGC GGCCCMWATC TNGTMAASAG      60
ATCTCGAAYT CGGCAAAAK ACGCMAYGTC AAGTGIRAYY CGGTACATA TONTGCGNG      120
TCAACMCERA AGCCGNGTCA CCGYTCCTCT GGGGCGCCAC CCCCACGGT RATGCAACTT      180
CGCGCGCCAC CGYCAAAAGG KTCWTRAGG CGCTAAAGGT CAMCAATTCC TEAGGTMCN      240
CACCGTTNTT TGGCCCGCCC RANTYCTTAC CCGCAATWTC GGTAAATCGG AATTGGGCGN      300
YCGGCTTGGG CAATAAGKTN TTGGSCAAGC GCGGWTCTYC NCTGGCCGGA ATTCCGNCAT      360
TCKTTTAACG SKTGRACCGT TTYCCCGGYT GCGGTAAYTG YTYCNTSGGC GCGYTCGCGC      420
CRMAGCASY YCCTAACGGY CMCCAGCCAA TACCKTTGGC TTTRAACCA CCGGATNAAY      480
TGKTACCCAC YTCASSGTS CTGRANTRE TMTCTGAA AANMCCACN AACCGGNTT      540
RATCTGCTTC MTCANCWTT SCCGGGTTCT GCCGTTTTGR AAYCTTNATC CMTYCAAAAG      600
GTTTAMTTTC CCAANRAAT CGGYTTGCGA CCTTGGCGCG GCGTGGTTM CGMWCCTTR      660
AMATCCNCCS GCGGCAAAAN AMTTSQNTT GCGCGGTCG CCGGAAATAT YCNTGCGCTT      720
GNAAATTGSS GGGATCCCGN GSGNAYCCGS CWTGCGGCK TCCCACTTG GWACAAATYC      780
WKGCGTTCCA AACCCGCGNC CCGGCGGTCG GCGGTTTTT CCMWNNAAA AAGKSTTGN      840
NYTTTTTCGG CMTAANTTCA CCGCKNTWT GGNCCNAAC YTYCLANTTC CANACCTTTA      900
AASAAANTYK YGKTYCCCG TTTTCCGCG SANCCCCCG NMSSNNCGG AAAAAAGNK      960
TYNGCCTTAN CNGNKTNTT TMTYCCCGC NMNNNSNMCT NCBKCKNRY NGNSNMNCTT      1020
MKYSKNNNNN SNNNNNNCGN GNCGSMKCM CMNNCNGMYK NGNKSNNCCC MSC      1073

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(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

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GNSNGNKNTH TMCAYCWYCT SCACSGGGTC TATTGCGGCG GCAATYTNCT CKASAGATCT      60
CGATYTCGGC AMNANAARTG TCGTCGTCAA TTTCAGKKTG GTCKTCAAAY GGGCCAGGCC      120
GNGACCRACA CCGTGNGTCA CCGAAAAAC CAACAGCWTG AAATWTCRAG GCGRAGGCGC      180
TRTCAATYCC CRASCARTTA ACCGTKTCW TCRAGGTGC CRAACCAGGC ACCCGYTCA      240
CGCGCGGSCA ANTGGCGCTG CCGGCGGNTT TCAGCTGAT TYCTGACCT RMTCTGTGGG      300
TGGYCAMENT GGTGAAGGCC CWCCCGCGA AGAACTGGAG GGCRAATTCC CAGGANCNA      360
GRAACTCNAG GAACCCGCGG TAKAANCCGG CRAAACCRAG GCGGYTGGCN ATTCCNATTA      420
NAMSGGTTTG CRACNTGGCT RAACCGTTT CTGCTCGGC CTCGGCAACC CTGGACCANT      480
TACCCCKTNC CCGGNNMAC CYCGGGTNCY TSKYCCCAAT NTGCTCCCGC GNRANTNGGC      540
CNAATTCCAG GGCNCCANCT TTCCGCGCG AATTCCCTTG GTTAATCACC GCGCNCNCTT      600
GGTTTTGGGC AACCCGCTYS CTTMTTTAAA CATTCGSSCC CAAATGGGNC STTGGGAAAT      660

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TCCTTYCGGT	GGGGCSGGCR	ANMYTTCTCT	YCCCAASAN	CTTAMYCCAN	TTGGSSNTCC	720
CGGKCAAAWE	NGGGGGGNA	AAGGGCCCCC	CGGNTSCGCC	GGGGKXGCC	CYGGKTTCAA	780
AANTTTCSGG	GTSTMSGG	NVTCSCCCCC	CSGCCAAGRA	CCGNGGTTTT	TTTTTGAACC	840
KCMANTCSEA	AMCCCCSSC	CCMAAAGGS	GCCTNAAWGR	RAYTTNKSOC	CNMAAACSGG	900
CCCCCAKTYV	SGGKTTGNHC	CNCCSGKLG	CGMTSTTMM	MRCCCTTTGN	GNKTTTTTAN	960
MGSCCTTNNC	CACCCCTYCK	GGGKCSMNA	GAATMYWKC	CNCGGGNNAN	RCSCCCCCNN	1020
GGGKGGGGK	MGAGYSCKT	CTGGCGNOM	YKNTTTCGCC	C		1061

(3) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNGNNXW	ATMCAYWYY	CTSCACCSG	GMTCWATTGC	GGCCGCWYV	TNCTMAASAG	60
ATCTMGAAFT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTCANAG	CTGTCAACGC	120
GGTGCCGCSG	GTGSTRASCA	CMCATTCGGR	AACACCAAAC	CCGTCCGCGG	GYCACCGGCK	180
TGCGCTGCAA	AAVCCCTCCG	GOCACCTYRA	AACAAYWYCT	CCTGCAACSC	ARSCCGTTYC	240
GGGGCCGGRAT	CCTGGKYCAS	YTCSCCTTGC	GGTGCGCCAA	GGTACTGGCS	CWYCRAMACC	300
GCTYCGGGBA	ACCMAACGTA	AATCTTGCCN	AATTTGCNTT	CCCCCTECCC	TTRATNAATT	360
TGTTAAACCA	CGCAAACTTY	CGGKXTCTC	CTCTGCCRA	WTCCGRWTCC	RATNYCGCCA	420
TGGCCTNNTC	KYCTYCKYCS	GTMCCTAAAT	CTTGSTATCC	TATATTGTCC	CTAAATGCRA	480
ATCTKGGCTG	TCCATNFGCT	GGCCTTCAAA	TTWAMANCAG	NGGTTTCTTY	CTTCNAAAC	540
CCSTTGGCCC	CAAAACCHAAA	AATGATNATA	ATAATGGTGC	TNTCAAACCC	CGCNCCTATY	600
CMATCSGKCC	AMMCCGGRON	GGTANCKGG	GHAAATCTMN	AACCCCAAGC	CATAASNTTG	660
SGANAAACCV	WNCNMGYCA	CCAAAACNMY	NTNNTTGGNY	SSNTTCGGMN	YCATGGCTTN	720
CMRAAACTTA	AAACTNMYG	GGYCCATATA	AAMMGGGYC	SAMCCGGAAG	WTTTTVTGN	780
KYNAAACCHN	AAKCTTTTTT	CHAACTTAN	WNTYCTNCC	RCRCMANTGG	CNSGGARTKT	840
SSSCTTNCCT	ATCKYCCMAA	AGNGGGRANA	CCARCCCCAA	TTCTTNNNTN	KNKNCCTNST	900
TRNAAAAGCG	GHNTYCNMAA	AAACNCTNCC	NKNTCTCCAA	AAKAMCCCTN	AAAGAKNTCN	960
NAANASXYEN	NNNSCCCCCC	CTMMN				986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGNNXN	ATMAYCWCT	SATYYACCSN	GGNNKWATTG	CGGCCRMANT	CTNGTMKASA	60
GATCTMGAAA	YTCGGCAAAG	AGYATXCTCG	GGGGCCAGAT	TNTTGGCCCC	CAACCCGCCG	120
ACTTTGCAYW	TCAACAKTCC	SGGTGCCCCA	AAAAANTCWT	ACCCCATMCC	TYCTTGCASH	180
ASYTGGCCCC	RATTRAACAC	CGGGCGGGCW	TGTTGGCCCA	GATATTYCAS	CAGYTCAAAY	240
YCTTTXTAGK	TAAATCTAG	CGGGCGGCCA	CNCAGCGGGG	CGGTETAGGT	GCTTYCTCA	300

ATMACCAGCT	CCCCAGGGV	CACCTTSCCC	AAAAYCTCCT	GGCTCAGCCA	AATTYCCGCS	360
CCGGCCCAACM	ACCANCCSCA	TYCTGGGNTC	AATCYCACCG	GGCCCCGTGY	TAAAMMAAMA	420
GRATCTCTTC	MANCCSCCAN	TCAGCSYTHA	CNGCMACAGC	CCGCTTCTCT	CAMACCCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACCTA	ACAGGCGGNC	AGGCTTCCOC	CGGANSAAAG	540
GTCTTACSCC	NNYAANRAAA	MAAGNTCTGT	TTTCCCCCTC	CASAASHAAA	AANCCCCSGC	600
CGGGCCCTTCN	NMMGGGTTTG	GGGMAHANA	AARCNCCGNN	GGAACGMATC	CGAAAMCTCC	660
CAAGTCNMT	TWAAACYCN	NNAACCCCCC	ANTTTTGGGA	AAGGNTCCOC	NTTMYCCCCC	720
TTTTASGHTS	GGGMYCTY	TAAAAAAT	CCCCAAAAAG	CCCCGGGAAG	GGTGMAMCTG	780
GGNAAATTC	CAAMCENWCK	TTTTTYNGGT	TMCGGGGGRA	AATTYCNCCTC	CCYYNNNGGG	840
CSSGSSNRAT	TAYGGMSMT	TTTNNAAWTM	NSGKTSAMM	YNNKCCMMNN	NNNMSMAHKK	900
TNAMCKCCCN	CCTCNGSKY	CSCYNCCCSG	GNAGNGGRAS	MKCCNANMAA	AYASGTTNKK	960
CGGAAMCMN	AATGNNMSC	CCGGASHCMN	NNNMAAATMT	CNCNKNNSNN	AANRGMBACN	1020
CCCNNSNGMN	RRGAARMTNY	YCCCCGSKM	GKGNKAAAAN	GKYCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NNNGNCHMT	MTACATOWTT	CTGCACCSGG	GNTCWANTGC	GGCCGCANKY	TTGTGASAG	60
ATCTCGAAYT	CGGCAMGAGG	ACWCTCCRA	CGCCCCACA	NACTCTGGGG	TGTGTACCC	120
ATTGNGCGCK	TCACGCGCCC	AYTSANCCAK	TNACTGGGG	TGCCCTYCC	CNTGCCCGG	180
GGCTTCACGG	CKCTSCWTCT	RAAGSCNTGG	CSCACCGCAT	TGGGTTTTCT	RAACGCTGG	240
AAANTGGCCA	GGCGTCTGGC	TCATGGGNTC	TACCAACGC	CNGCCCCCAA	CRCTTTCTTA	300
AATCCGGYCC	NTCCTGANC	CTTTGAAYCC	CGGGGSRAGA	ACTGGTTGCS	CNCGAYCTGC	360
TGGAACCTTK	TENAAATCC	GCANAKTGT	TENTAMGYCC	CNCCGGAAGG	NGAACCTACT	420
TTGCGWANG	TGGGCKKCC	GGCCTTATCA	STCCTGATCA	ACGGGGAAGT	GGYNNSTTG	480
KGGGAAAAAG	RECTCAATG	MTYGGTECK	GCTGGKANC	CGSCCCTGK	GYCCNAATG	540
GAAGGCSMAG	GGTTAANGCC	MTTYCNYCC	NSCCGTSTGA	SGNTTYCCG	MGGANKAMNN	600
NNKIAMWTTK	TCRNGGGCCW	ATSTCCCGG	CKSTTAKAGA	ANACTYCCW	WCCGNTYSC	660
SAAAGNTKCS	GCGMTTPTS	SCCMGANGN	YCTGATTTTA	GGGGGKYKCC	CCCCGGGTYC	720
CGAAWNRKY	CTYAGGGGSM	GFYCSAGCSC	CGMNATNAG	AGNAAGGKTT	RYGTSKNC	780
TYTNEGGAAC	WSCNNCNSAK	ANAACNNKKT	TCCSCCNTMS	AGNKTNKGT	YCCNKTSTTC	840
TAAGAGGAGC	TATNKCSCC	CKTGANGMM	GAGWGMGCC	KYCCCSHKRT	TCTNGWAAA	900
TATKAGMGG	TKCCGMAGMK	CCSCGTTTT	TRYGANAAMN	MSMRKHKKTG	CGMYTCTSC	960
GGGNTTTGTA	GAGTAKTCGS	CSCSMWGAC	WCSGCMGNG	AGYKKTSTTS	YANTGARCGY	1020
MNNSKTMKMT	MECECGGONA	GGAGNGCCCC	CSANEMSTGY	NEGGMSNSG	ARAKGATGGS	1080
GGCCNCGMN	MCMGGANMGA	SANNGMGGMR	GGGGGKTGNC	TCXSCCGNS	CSANGRAGAA	1140
GKTCNGSCGC	CGMGGKYGKT	KTKTKNTG	YETCMSSMM	NAGAAAAGAG	AGGCC	1195

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTCGCLACT	AGCATGSCAG	TGGGAACGAT	GGCCTCATTC	AGCATTTCGA	60
TGGTTTGTTC	AAAACCGSAC	ATGGCACTCC	AGTCGCTTTC	CGCTTCGGCT	ATCGGCTGAA	120
TTTGATTGCG	AGTGAGATAT	TTATGCGAGC	CAGCCAGAGC	CAGACGGGCC	GAGACAGAAC	180
TTAATGGGCC	CGCTAACAGC	GCGATTTCCT	GOTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTY	GATGGGTGTC	TGCTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCAC	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTTTACA	GGCTTCGAGC	CCGCTTCGTT	CTACCATGSA	CACCACGACG	CTGSCACCCA	480
GTTGATCGGC	GCGAGATTTA	ATCGCCGCGA	CAATTTCGGA	CGCGCGCTGC	AGGSCCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTCGCGCGC	CAGTTTGTGT	GCCACCGCGT	600
TGGGAATGTA	ATTGAGCTCC	GGCATCGCGC	GTTCGACTTT	TTCCCGCGTT	TTCCGAGAAA	660
CGTGCGCTGC	CTGCTTCACC	ACCGCGGAAA	CGCTCTGATA	AGAGACACCG	GCATACTCTG	720
CGACATCTTA	TAACCTTACT	GGTTTCACAT	TCACCACTCT	GAATTCAGCT	TCTTCGCGGC	780
GCTATCATGC	CATACCGCGA	AAGGTTTTGC	GGCATTCGAT	GCTGTCGCGG	ATCTGCGACG	840
TCTCGCTTAT	GCGACTCTTG	CATTAGGAAG	CAGCCGAGTA	GTAGGTTGAG	GGCTTTCAGC	900
ACCGCGCGCG	CAAGGAATGG	TGCATGCAAG	GAGATGCGGC	CCAACAGTCC	CCCGGCCACG	960
GGGCTTGCGA	CCATACCCAC	GGGAAACAA	GGCTCATGSA	GGCGAAGTGA	GCGAGCGCGA	1020
TCTTCCCGAT	CGGTGATGTC	GGCGATATAG	GGCCAGCAAA	CGGCACCTGT	GGCGCGCGTG	1080
ATGCGCGCGA	CGATGCGTCC	GGCTTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	1140
GACTCACTAT	AGGGGAATTC	TGAGCGGATA	ACAATTCCCG	TCTAGAAATA	ATTTTGTGTTA	1200
ACTTTAGAAA	CGAGATATAC	ATATGGGCGA	TCATCATCAT	CATCACTGSA	TGCACATCAT	1260
CGGGACGAGC	CCCACATCTT	GGGAACAGGC	GGCGCGCGAG	GGCGTCCAGC	GGCGCGCGGA	1320
TAGCTTCGAT	GACATCGCGC	TGCGTCGGGT	CATTCAGCAG	GACATGCGCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTGSA	AGTGTCTGTC	AAGATGAGGC	CGGCGCAACT	1440
GAGGGCGCTG	AAACCACCGA	GGGTTTCGCG	TGAAACCGGC	GGCGCGCGCG	GTACTGTGCG	1500
GACTACCGCG	GGCTCGTCCG	CGGTGACGTT	GGCGAGACCC	GCTAGCACCG	TGCTCTACCG	1560
GCTGTTTCAC	CTGTGGGCTC	CGGCTTTTCA	CGAGAGGTAT	CGGAACGTCG	CGATCACCGC	1620
TCAGGCGCAC	GGTTCTGGTG	CGGGATCGCG	GCAGGCGCGC	GGCGGAGCGG	TCACATTCGG	1680
GGCTTCGAGC	GGTATCTGT	CGGAAGGTGA	TATGGCGCGC	CACAGCGCGC	TGATGAACAT	1740
CGGCTAGCGC	ATCTCGGCTC	AGCAGGTCAA	GTACAACCTG	CGCGGAGTGA	GGCGGCACCT	1800
CAAGCTGAAC	GGAAAAGTCC	TGGCGGCGAT	GTACCAGGGC	ACCATCAAAA	CCTGGGACGA	1860
CGTCGAGATC	GCTGCGCTCA	AGCCCGGCTT	GAACCTGCGC	GGCACCGCGG	TAGTTCCGCT	1920
GGAGCGCTCC	GACGGGTGCG	GTGACACCTT	CTTGTTCGCG	CAGTACCTGT	CCAAGCAAGA	1980
TGCGAGGCGC	TGGGGAAGT	CGCCCGGCTT	CGGCACGACG	GTGCACTTCC	CGCGGCTGCT	2040
GGGTGCGCTG	GCTGAGAACG	GCAACGGCGG	CATGCTGAGC	GGTTGCGCGG	AGACACGCGG	2100
CTGCTTGGCG	TATATCGCGA	TCAGCTTCTT	CGACGAGGCT	AGTCAACCGG	GACTCGGCGA	2160
GGCCCACTGA	GGCAATAGCT	CTGGCAATTT	CTTGTTCGCG	GACGCGCAAA	GCATTGAGGC	2220
CGCGGCGGCT	GGTTTCGCGT	CGAAAACGCT	GGCGAACCGG	GGCAATTCGA	TGATCGACCG	2280
GGCGCGCGCG	GACGCTTACC	CGATCATCAA	CTACGAGTAC	GGCATGCTCA	ACAACCGGCA	2340
AAAGGACCGC	GCCACCGCGC	AGACCTTGCA	GGCAATTCG	CATGCGCGCA	TCACCGACCG	2400
CAACAGGCGC	TGTTTCCTCG	ACCAGGTTCA	TTTCCAGCGC	CTGCGCGCGC	CGTGTGTA	2460
GTGCTCTGAC	GCTTGATCG	CGACGATTC	CAGCGCTGAG	ATGAAGACCG	ATGCGCGTAC	2520
CGTCCGCGAG	GAGGCAAGTA	ATTTGAGCGC	GATCTCGCGC	GACCTGAAAA	CCGAGATCGA	2580
CCAGGTGGAG	TGACCGCGAG	GTTCGTTGCA	GGCGCAGTGG	CGCGCGCGCG	CGCGGACCGC	2640
CGCCAGGCGC	GCGGTGCTGC	GCTTCCAAAG	AGCAGCCAA	AAGCAGAACG	AGGAAGTCCA	2700
CGAGATCTCG	ACGAATATTC	GTGAGGCGCG	CGTCCAAATC	TCGAGGCGCG	ACGAGGAGCA	2760
GCAGCAGGCG	CTGCTCTCGC	AAATGGGCTT	TGGATTGAGC	TTCCCGCTGC	CTGCTGGCTG	2820
GGTGGAGTCT	GACGCGCGCG	ACTTCGACTA	CGGTTGAGCA	CTGCTCAGCA	AAACCACCGC	2880
GGACCGCGCA	TTTCCCGGAC	AGCGCGCGCG	GCTGCGCAAT	GACACCGCTA	TGCTGCTCGC	2940
CGGCTAGAGC	CAAAAGCTTT	ACGCGAGCGC	CGAAGCGACG	GACTCCAAGG	CGCGCGCGCG	3000
GTTCGCGCTG	GACATGGGTC	AGTTCTATAT	GCTTACGCG	GGCACCGCGA	TCACCGAGCA	3060

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AACCGTCTCG CTYGACGCCA ACGGGGTGTC TCGAAGCGCG TCGTATTACG AAGTCAAGTT 3128
CAGCGATCCG AGTAAGCCGA ACGGCCAGAT CTGACCGGGC GTATTCGGCT CGCCCGCGGC 3180
GAACGKACCG GACGCCGGGC CCGCTCAGCG CTGCTTTGTC GTATGGCTCG GGACCGCCCA 3240
CAACCCGGTG GACAAGGGCG CGGCCAAGGC GCTGGCCGAA TCGATCCGGC CTTTGGTCGC 3300
CCCGCCCGCG GCGCTGGCGG GGGAGTCCG TCTACCCCG AGGACACCGA CAGCGCAGCG 3360
GACCTTACCG GCGTGAGAA TCTGCGATA TCCATCACAC TGGCGCCGCG TCGAGCACCA 3420
CCACCACCGC CACTGAGATC CCGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTGC 3480
TGGCACCGCT GAGCAATAAC TAGCATAACG CCTTGGGGCG TCTAACGGG TCTTCAGCGG 3540
TTTTTTGCTG AAAGGAGGAA CTATATCCGG AT 3572

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
 1             5             10             15
Asp Gly Xaa Arg
          20

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
 1             5             10

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg

```

1 § 10

(2) INFORMATION FOR SEQ ID NO:348:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Asp Ala Gly Lys Asa Ala Gly Asa Asp Val Asa Arg
1 3 10

(2) INFORMATION FOR SEQ ID NO: 347:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(22) MOLECULE TYPE: nucleoside

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 247.

Thr Asa Glu Glu Asa Glu Glu Ser His Asn Ser Ala Ala Val Gly Asn
1 5 10 15
Asa Lys

(2) INFORMATION FOR SEQ ID NO:148:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(4) MOLECULE TYPE: Other

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CTAGTACGTA CTCAGTCCCA GACCGTG

5.

(2) INFORMATION FOR SEQ ID NO: 349:

(4) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTACGGA ATTCACTTCC ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCG	ATCATCATCA	TCATCACCTG	ATCGACATCA	TGGGACCCAG	CCGCACATCC	60
TGGGAACAGG	CGGCGGCGGA	GGCGGTCCAG	CGGGCGCGGG	ATAACGTCGA	TGACATCCGC	120
GTCGCTCGGG	TCATTTAGCA	GGACATGGCC	GTGGACAGCG	CCGCCAAGAT	CACCTACCGC	180
ATCAAGCTCG	AAGTGTGCTT	CAAGATGAGG	CCGGCGCAAC	CGAGGGGCTC	GAACCCACCG	240
AGCGTTCCG	CTGAACCGGG	CGCGGGCGCC	GCTACTGTCC	CGACTACCCC	CGCGTCTCCG	300
CGCGTACCT	TGGCGGAGAC	CGGTAGCAGG	CTGCTCTACC	CGCTGTTCAA	CTGTGGGGT	360
CGCGCTTTTC	ACGAGAGGTA	TCCGAACCTC	ACGATCACCG	CTCAGGGCAC	CGGTTCTGGT	420
GCCGGGATCG	CGCAGGCTCC	CGCGGGGACG	GTCAACATTG	GGGCTCCGA	CGCTATCTG	480
TCCGAAGGTC	ATATGGCCGC	GCACAAGGGG	CTGATGAACA	TCCCGCTAGC	CATCTCCGCT	540
CAGCAGGTCA	ACTACAACTT	GGCGGAGTG	AGCGAGCACC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGCGGCCA	TGTACGAGGG	CACCATCAAA	ACCTGGGACG	ACCCGCAGAT	CGCTGCGCTC	660
AACCCCGGCG	TGAACCTGCC	CGGCACCGCG	GTAGTTCCGC	TGCACCGCTC	CGACGGGTCC	720
GGTGACACTT	TCTTGTTTAC	CGAGTACTTG	TCCAAGCAAG	ATCCCGAGGG	CTGGGSCAAG	780
TGGCCCGGCT	TGGGACCCAC	CGTCCACTTC	CCGGCGGTGC	CGGGTGCCCT	GGGTGAGAAC	840
GGCAACCGCG	GCATGGTGAC	CGGTTGGGCC	GAGACACCGG	GCTGCGTGGC	CTATATCGGC	900
ATCAGCTTCC	TGACCCAGGC	CAGTCAACCG	GGACTCGGCG	AGGCCCAACT	AGGCAATAGC	960
TCTGGCAATT	TCTTGTTGCT	CGACCGCGCA	AGCATTGAGG	CGCGGGCGGC	TGGTTCTCCA	1020
TCCAAAACCC	CGGCCAAGCA	GGCGATTTCG	ATGATCGAGC	GGCCCCCCCC	GGACGGCTAC	1080
CCGATCATCA	ACTACGAGTA	CGCATCTCTC	AACCAACCGC	AAAAGGACCG	CGCCACCGCG	1140
CAGACCTTGC	AGGCATTTCT	CGACTGGGCG	ATCACCGAGC	GCAACAAGGC	CTGTTCTCTC	1200
GACCAGGTC	ATTTCCAGGC	GCTGCGGCCC	GCCTGCTGTA	AGTTGTCTGA	CGCGTTGATC	1260
CCGACGATTT	CCAGCGCTGA	GATGAAGACC	GATGCGCGTA	CTTTCGCGCA	GGAGGCAGGT	1320
AATTTCSAGC	GGATCTCCGG	CGACTTGAAA	ACCCAGATCG	ACCAGGTGGA	GTCCAGCGCA	1380
GGTTCTTTGC	AGGGCCAGTG	GCGCGGCGCG	CGCGGGAAGG	CGGCCAGGTC	CGCGGTGGTG	1440
CGCTTCCAAG	AAGCAGCCAA	TAAGCAGAAG	CAGGAACCTG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGCGG	GGGTCCAAAT	CTCGAGGCGC	GACGAGGAGC	AGCAGCAGGC	GCTGTCTCTG	1560
CBAATGGGCT	TTGTGCCCCAC	AACGGCGCGC	TGCGCGCGCT	CGACCGCTGC	AGCGGACCGC	1620
GCACCGGCGA	CACCTGTTTC	CGCGCCACCA	CGCGCGCGCG	CGAACACCGC	GAATGCCCAG	1680
CCGGCGGATC	CCAACGTCAG	ACCTCGCGCG	GCGGACCGGA	AGGCACCGCC	GCCACCTGTC	1740
ATTGCCCCCA	ACGCACCCCA	ACCTGTCCCG	ATCGACAACC	CGGTTGGAGG	ATTGAGTTTC	1800
GGCTGCGCTG	CTGGCTGGGT	GGAGTCTGAC	GCGCGCCACT	TGCACTACCG	TTGAGCACTC	1860
CTCAGCAAAA	CCACCGGGGA	CCCGCATTTT	CCCGGACAGC	CGCGCGCGGT	GGCCTAATGAC	1920
ACCCGTATCG	TGCTCGGCGG	GCTAGACCAA	AAGCTTTTAC	CCAGCGCGGA	AGCCACCGGAC	1980
TCCAAGGCGG	CGGCGCGGTT	GGGCTCGGAC	ATGGGTGAGT	TCTATATGCC	CTACCCGGGC	2040
ACCCGGATCA	ACCAGGAAGC	CGTCTCGCTC	GACGCCAAGC	GGGTGTCTGG	AAGCGGCTCC	2100
TATTACGAAG	TCAAGTTTCA	CGATCCGAGT	AAGCCGAAGC	GTCAGATCTG	GACGGGGGTA	2160

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ATCGGCTCGC CCGCGCGGAA CCGACCGGAC GCGGGGCCCC CTCAGCGCTG GTTTGTGGTA 2220
TGGCTCGGGA CCGCCAACAA CCGGTGGAC AAGGGCGCGG CCAAGGCGCT GCGGAATCG 2280
ATCGGCGCTT TGGTGGCCCC GCGCGCGGCG CCGGCACCGG CTCCTGCAGA GCGGCTCGG 2340
GCGCTGGCGC CCGCGCGGGA AGTGGCTCTT ACCCGGACGA CACCGACACC GCAGCGGACC 2400
TTACCGGCTT GA 2422

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(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Met Gly His His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1             5             10             15
Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
 20             25             30
Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35             40             45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50             55             60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65             70             75             80
Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85             90             95
Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100            105            110
Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Gln Arg Tyr Pro Asn
115            120            125
Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130            135            140
Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145            150            155            160
Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165            170            175
Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
180            185            190
Leu Lys Leu Asn Gly Cys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
195            200            205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
210            215            220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225            230            235            240
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
245            250            255
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
260            265            270
Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
275            280            285
Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp

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290		295		300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala		Gln Leu Gly Asn Ser Ser		
305		310		320
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser		Ile Gln Ala Ala Ala Ala		
	325		330	335
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln		Ala Ile Ser Met Ile Asp		
	340		345	350
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile		Asn Tyr Glu Tyr Ala Ile		
	355		360	365
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr		Ala Gln Thr Leu Gln Ala		
	370		375	380
Phe Leu His Trp Ala Ile Thr Asp Gly Asn		Lys Ala Ser Phe Leu Asp		
	385		390	400
Gln Val His Phe Gln Pro Leu Pro Pro Ala		Val Val Lys Leu Ser Asp		
	405		410	415
Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu		Met Lys Thr Asp Ala Ala		
	420		425	430
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu		Arg Ile Ser Gly Asp Leu		
	435		440	445
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr		Ala Gly Ser Leu Gln Gly		
	450		455	460
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala		Gln Ala Ala Val Val Arg		
	465		470	475
Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln		Glu Leu Asp Glu Ile Ser		
	485		490	495
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr		Ser Arg Ala Asp Glu Glu		
	500		505	510
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly		Phe Val Pro Thr Thr Ala		
	515		520	525
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro		Pro Ala Pro Ala Thr Pro		
	530		535	540
Val Ala Pro Pro Pro Pro Ala Ala Ala Asn		Thr Pro Asn Ala Gln Pro		
	545		550	560
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala		Asp Pro Asn Ala Pro Pro		
	565		570	575
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln		Pro Val Arg Ile Asp Asn		
	580		585	590
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro		Ala Gly Trp Val Glu Ser		
	595		600	605
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala		Leu Leu Ser Lys Thr Thr		
	610		615	620
Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro		Pro Val Ala Asn Asp Thr		
	625		630	635
Arg Ile Val Leu Gly Arg Leu Asp Gln Lys		Leu Tyr Ala Ser Ala Glu		
	640		645	650
Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu		Gly Ser Asp Met Gly Glu		
	655		660	665
Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile		Asn Gln Glu Thr Val Ser		
	670		675	680
Leu Asp Ala Asn Gly Val Ser Gly Ser Ala		Ser Tyr Tyr Glu Val Lys		
	685		690	695
Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln		Ile Trp Thr Gly Val Ile		
	700		705	710
Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala		Gly Pro Pro Gln Arg Trp		
	715		720	725
	725		730	735

273

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
      740              745              750
Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
      755              760              765
Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
      770              775              780
Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Glu Arg Thr Leu
      785              790              795              800
Pro Ala

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACCG

34

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CCCTCCGAAT TCACCTCCGG AGGAAATCGT CCGCATC

37

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

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CATATGGGCC ATCATCATCA TCATCAAGGA TCCAAACCCAC CGAGCGGTTT GCCTGAAACG      60
GGCGCCGGCG CCGGTACTGT CCGGACTACC CCGCGGTCTGT CGCCGCTGAC GTTGGCCGGAG      120
ACCGTAGCA CCGTCTCTTA CCGCTCTTC AACCTGTGGG GTCCGCGCTT TCACGAGAGG      180
TATCCGAACG TCACGATCAC CCGTCAGGCG ACCGGTTCTG GTGCGCGGAT CGGCGAGGCC      240

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GCGGCGGGGA CGGTCAACAT TGGGGCTTCC GACGCCATATC TGTCCGAAGG TGATATGGCC 300
GCGCACAAAGG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC 350
CTGCCCGGAG TGAGCGAGCA COTCAAGCTG AACGGAAAAA TCCTGGCGGC CATGTACCAG 420
GGCACCATCA AAACCTGGGA CGACCCGAG ATCGCTCGGC TCAACCCCGG COTGAACCTG 480
CCCGGCACCG CGGTAGTTCC GCTGCACCGC TCGACGGGT CCGGTGACAC CTTCTTGTTC 540
ACCCAGTACC TGTCCAGCA AGATCCCGAG GCGTGGGGCA AGTCGCCCCG CTTGGGCACC 600
ACCTTCGACT TCCCGCGCGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG 660
ACCGGTTGCG CCGAGACACC GCGCTCGGTG GCCTATATCG GCATCAGCTT CCTCGACCAG 720
GCCAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTC 780
CCCGACGGGC AAAGCATTCG GCGCGCGGCG GCTGGCTTCG CATCGAAAAA CCGCGCGAAC 840
CAGGCGATTT CGATGATCGA CCGGCCCCCG CCGACCGCTT ACCCGATCAT CAACTACGAG 900
TACGCCATCG TCAACAACCG GCAAAAGGAC GCGGCCACCG CGCAGACCTT GCAGGCTTTT 960
CTGCACTGGG CGATCACCAG CGGCACAG AGCTCGTTCC TCGACCAGGT TCATTTCCAG 1020
CGCTTCGGCG CCGCGGTGGT GAAGTTGTCT GACGGGTGGA TCGCGACGAT TTCTTCGGGA 1080
GTTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGGCCAC AACGGCGGCC 1140
TCGCGCGCGT CGACCGCTGC AGCGCCACCC GCACCGCGGA CACTGTGTTC CCGCCGACCA 1200
CCGCGCGCGG CCAACACGCG GAATGCCAG CCGGGCGATC CCAACGCAGC ACCTCGCGCG 1260
GGCGACCGGA ACCACCGCGG GGCACCTGTC ATTGCCCCAA ACSCACCGCA ACCTGTCCGG 1320
ATCGACACCG CGGTGGAGG ATTGAGCTTC GCGTGGCTG CTGGCTGGGT GGAGTCTGAC 1380
GCGCGCCACT TCGACTACCG TTCAGCACTC CTCAGCAAAA CCACCGGGGA CCGCCCATTT 1440
CCCGACACCG CCGCGCGCGT GCGCATGAC ACCGTATCG TGCTCGCGCG GTTAGACCAA 1500
AAGCTTTACG CCAGCGCGCA ACCACCGGAC TCGAAGGCGG CCGCGCGGTT GGGCTCGGAC 1560
ATGGGTGAGT TCTATATGCC CTACCGGGCG ACCCGGATCA ACCAGGAAAC CGTCTCGCTC 1620
GACGCCAACG GGTGTGTGCG AAGCGCGTCC TATTACGAG TCAAGTTTCA GATTCGAGT 1680
AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGCTCGC CCGCGCGCAA CCGACCGGAC 1740
GCCGCGCGCG CTCAGCGCTG GTTGTGTGTA TGGCTCGGGA CCGCCACCAA CCGGTGGGAC 1800
AAGGGCGCGG CGAAGCGCGT GCGCGAATCG ATCGCGCTT TGGTGGCGCG CCGCGCGGCG 1860
CGCGCACCGG CTCTGACAGA GCGCGCTTCG GCGCGCGCGC CCGCGCGGGA AGTCGCTCTT 1920
ACCGCGACGA CACCGACACC GCAGCGGACC TTACCGCGCT GA 1962

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(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Gly His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
1           5           10           15
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
20           25           30
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
35           40           45
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
50           55           60
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
65           70           75           80
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
85           90           95
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

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100	105	110
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys		
115	120	125
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr		
130	135	140
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
145	150	155
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
160	165	170
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly Thr Gly		
175	180	185
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
190	195	200
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu		
205	210	215
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
220	225	230
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
235	240	245
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe		
250	255	260
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
265	270	275
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn		
280	285	290
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
295	300	305
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
310	315	320
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu		
325	330	335
Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly		
340	345	350
Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr		
355	360	365
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro		
370	375	380
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala		
385	390	395
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro		
400	405	410
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser		
415	420	425
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp		
430	435	440
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro		
445	450	455
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg		
460	465	470
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala		
475	480	485
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro		
490	495	500
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val		
505	510	515
	520	525
	530	535
		540

276

Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
545					550					555					560
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
			565							570					575
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
			580					585						590	
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Gln
		595					600					605			
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro
	610					615					620				
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr
625					630					635					640
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
			645						650						

CLAIMS

1. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128) and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative

substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

3. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341 or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. An expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A pharmaceutical composition comprising one or more polypeptides according to any one of claims 1-4 and a physiologically acceptable carrier.
10. A pharmaceutical composition comprising one or more DNA molecules according to claim 5 and a physiologically acceptable carrier.
11. A pharmaceutical composition comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a physiologically acceptable carrier.
12. A vaccine comprising one or more polypeptides according to any one of claims 1-4 and a non-specific immune response enhancer.
13. A vaccine comprising:
 - a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
 - a non-specific immune response enhancer.
14. A vaccine comprising:
 - one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

a non-specific immune response enhancer.

15. The vaccine of claims 12-14 wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine comprising one or more DNA molecules according to claim 5 and a non-specific immune response enhancer.

17. A vaccine comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a non-specific immune response enhancer.

18. The vaccine of claims 16 or 17 wherein the non-specific immune response enhancer is an adjuvant.

19. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 9-11.

20. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 12-18.

21. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

22. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6.

23. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO:155).

24. A pharmaceutical composition comprising a fusion protein according to any one of claims 21-23 and a physiologically acceptable carrier.

25. A vaccine comprising a fusion protein according to any one of claims 21-23 and a non-specific immune response enhancer.

26. The vaccine of claim 25 wherein the non-specific immune response enhancer is an adjuvant.

27. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 24.

28. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to claims 25 or 26.

29. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides according to any one of claims 1-4; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

30. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

31. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308,

310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

32. The method of any one of claims 29-31 wherein the immune response is induration.

33. A diagnostic kit comprising:

(a) a polypeptide according to any one of claims 1-4; and
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

34. A diagnostic kit comprising:

(a) a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

35. A diagnostic kit comprising:

(a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

36. A diagnostic kit comprising:

- (a) a fusion protein according to any one of claims 21-23; and
- (b) apparatus sufficient to contact said fusion protein with the dermal cells of a patient.

37. A fusion protein according to claim 23 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 153, 209, 351 and 355.

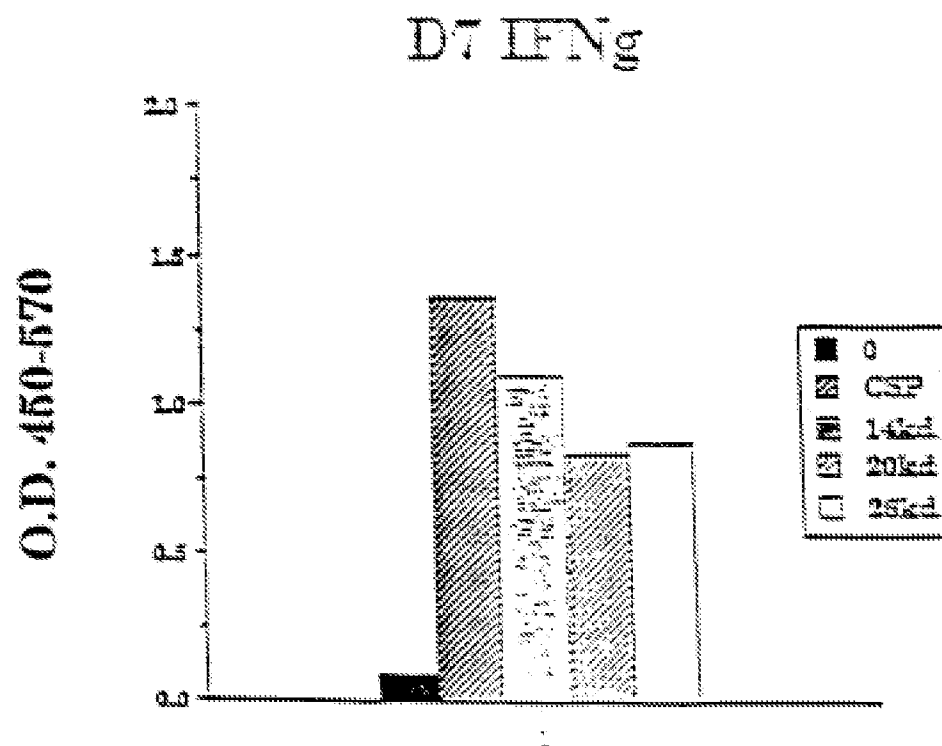
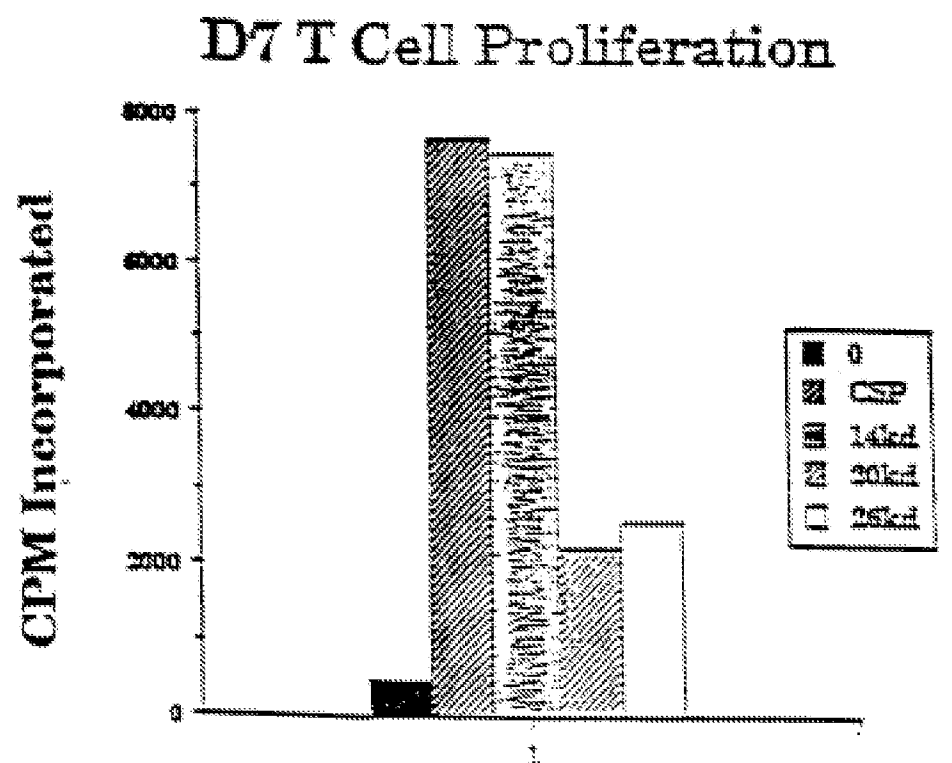


FIG. 12

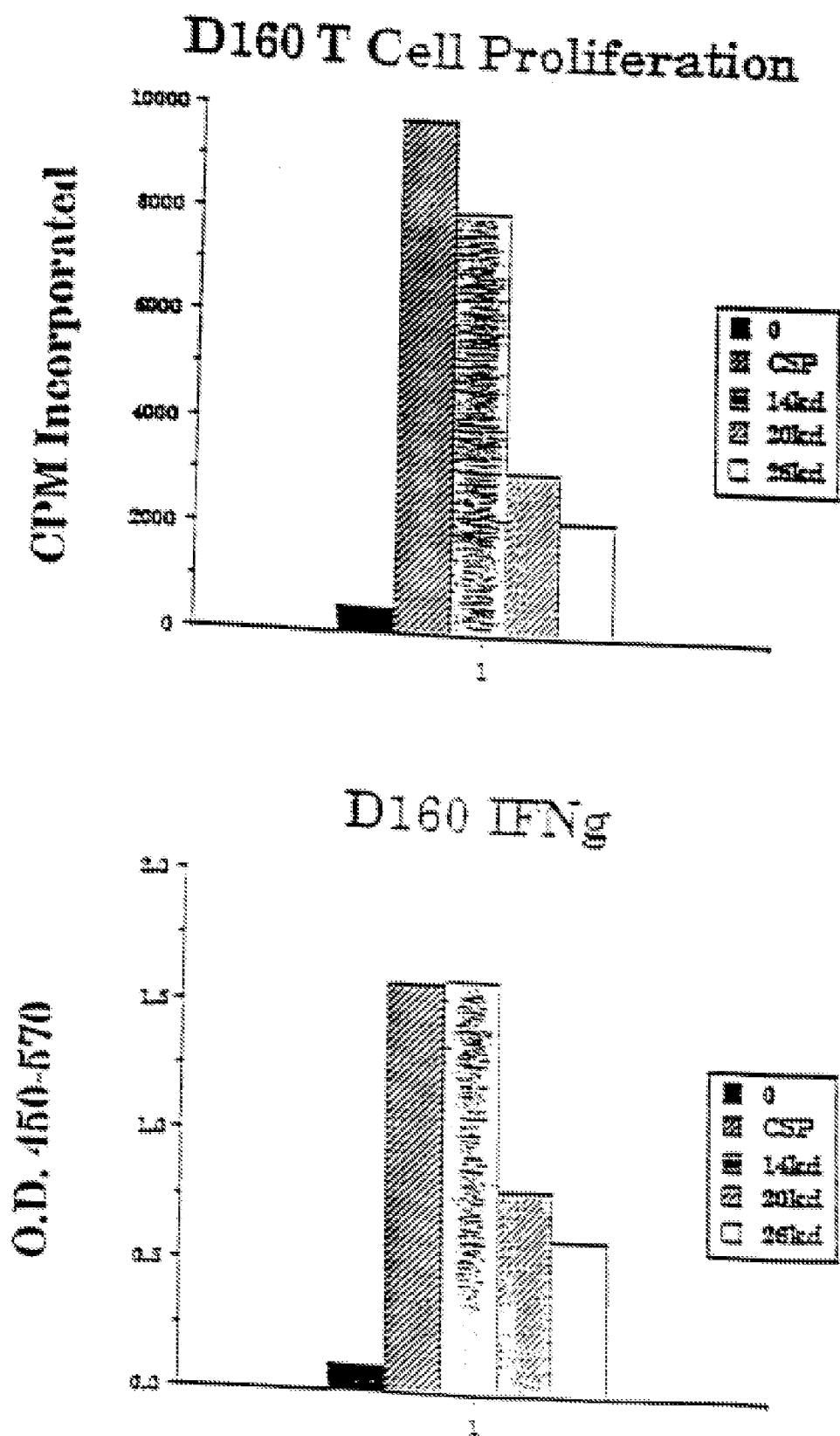


FIG. 1B

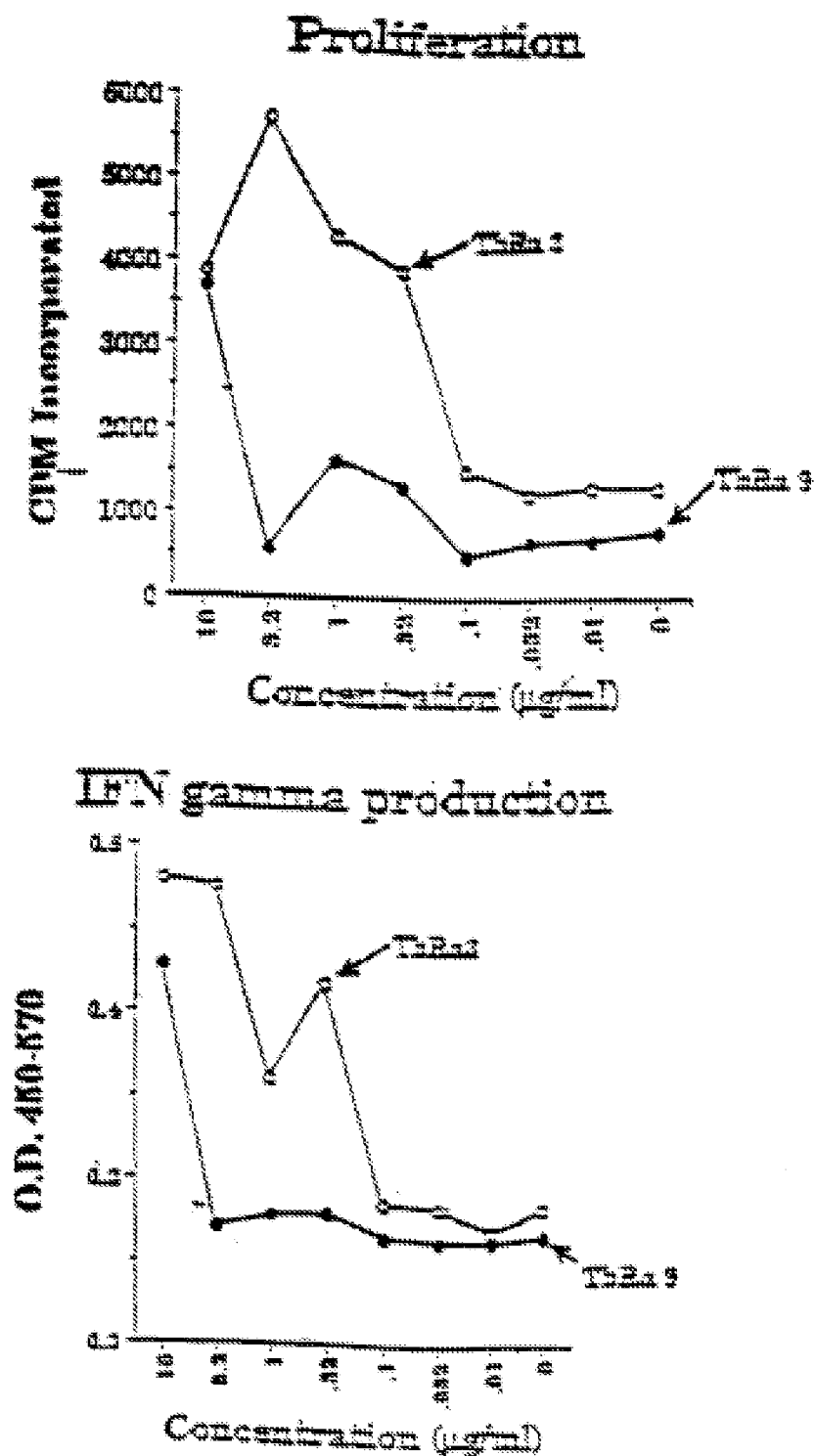
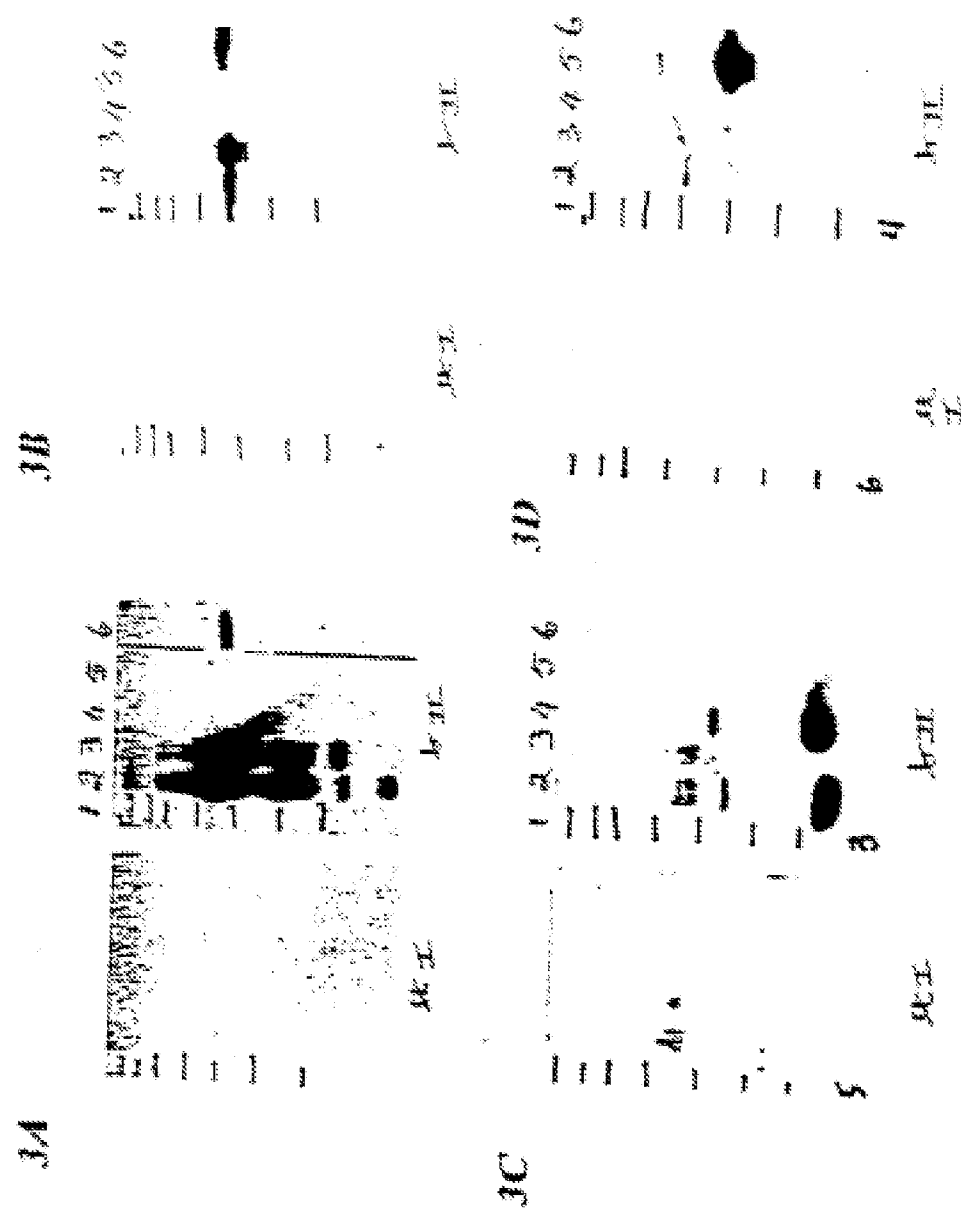


FIG. 2



FIGS. 3A-D

T cell clone 131TbH9 responds poorly to CSP

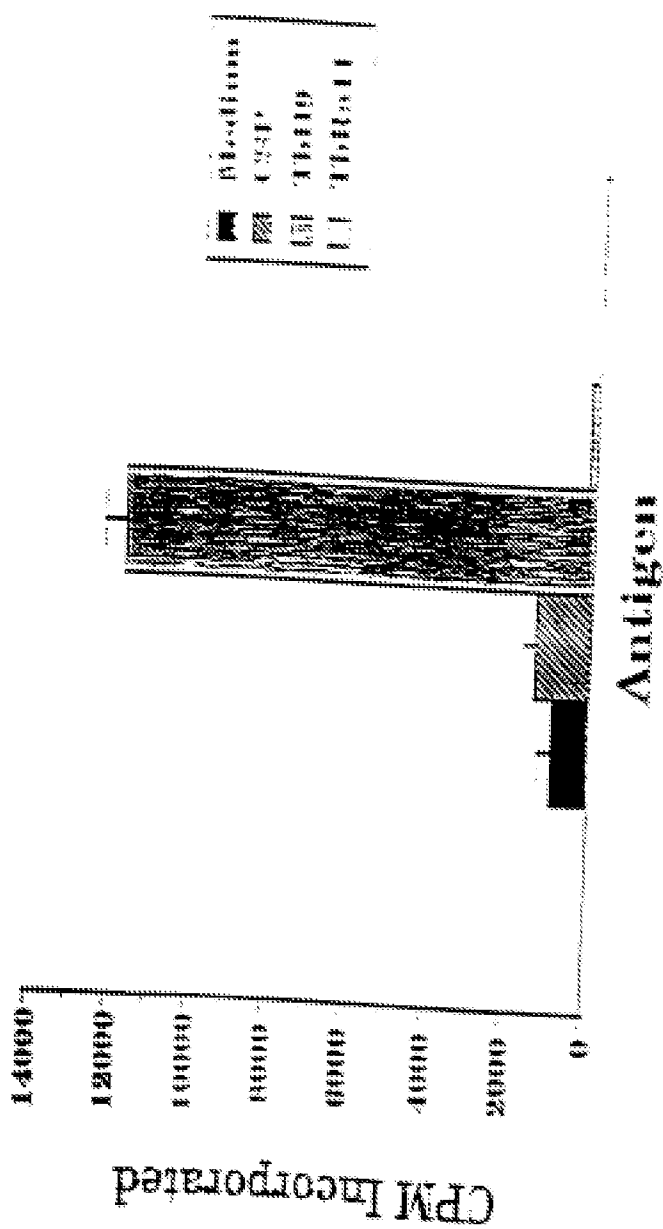


FIG. 4A

T Cell Clone PPD 800-10 IFN γ Production

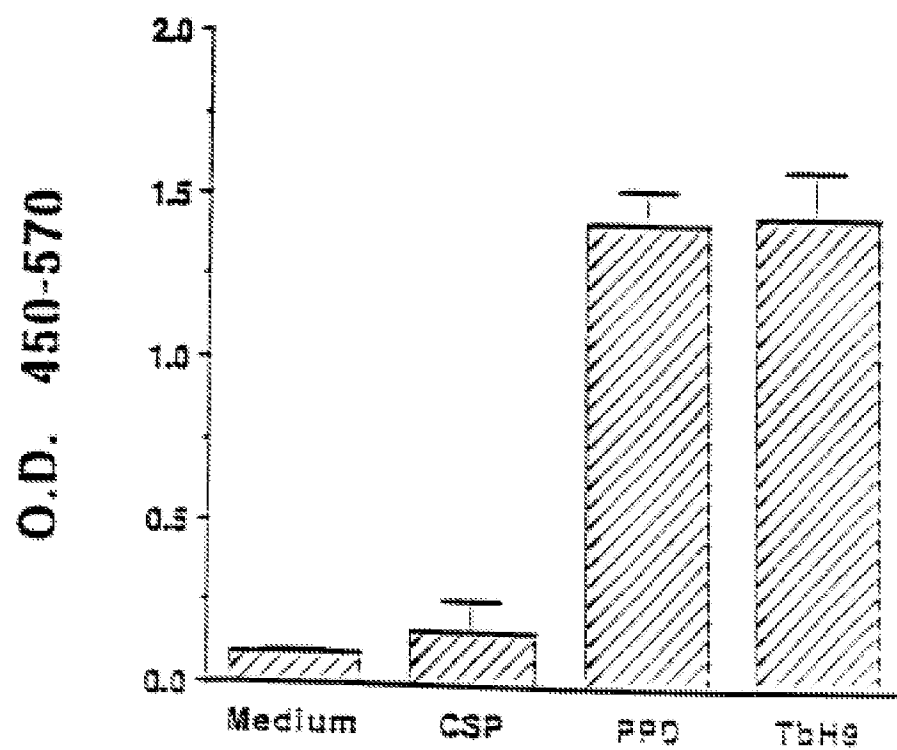
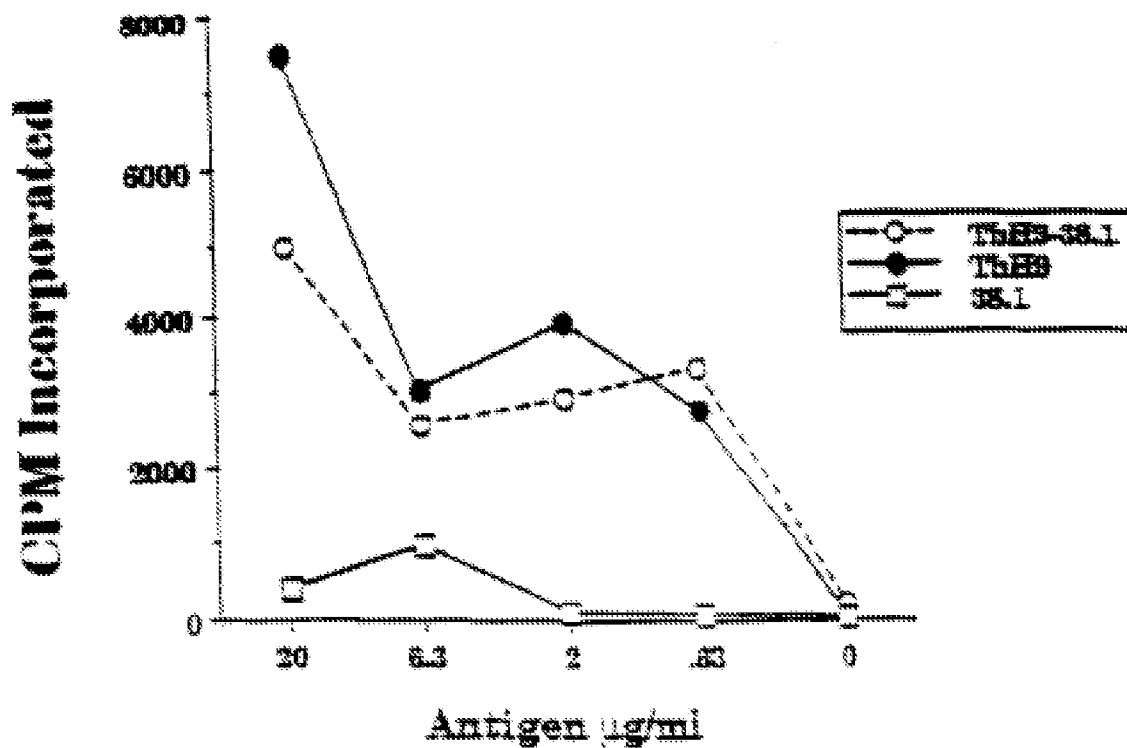
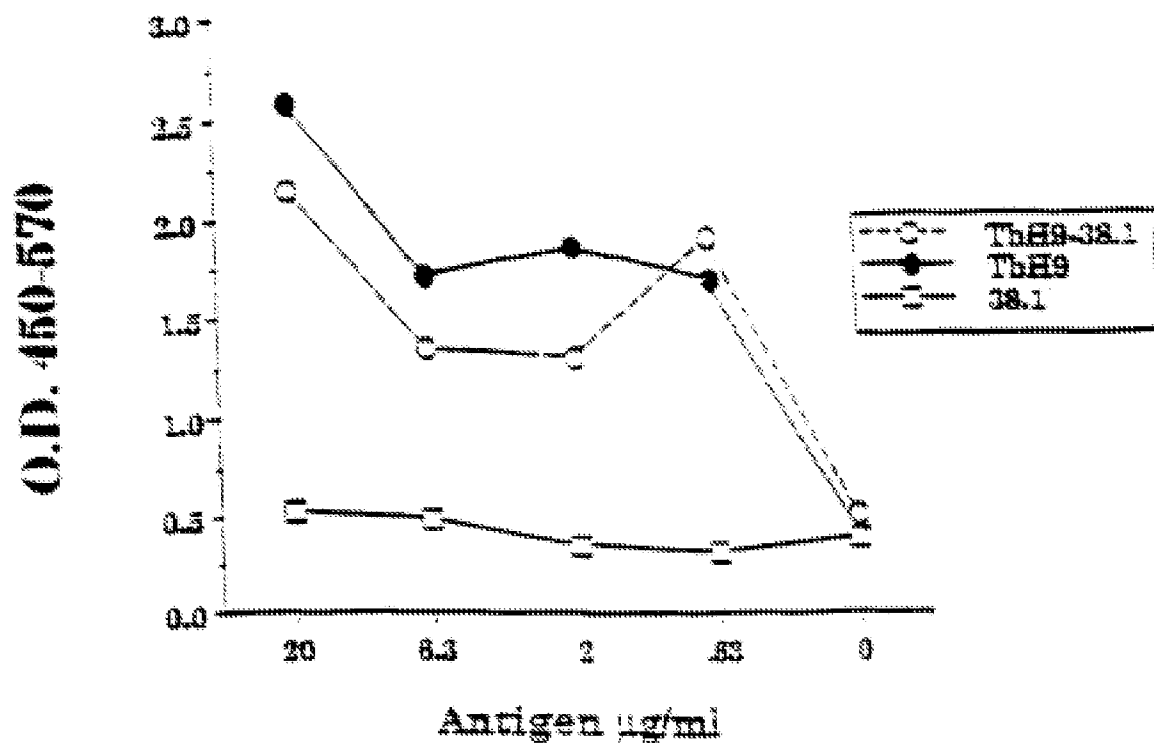


FIG. 4B

D131 T Cell Proliferation

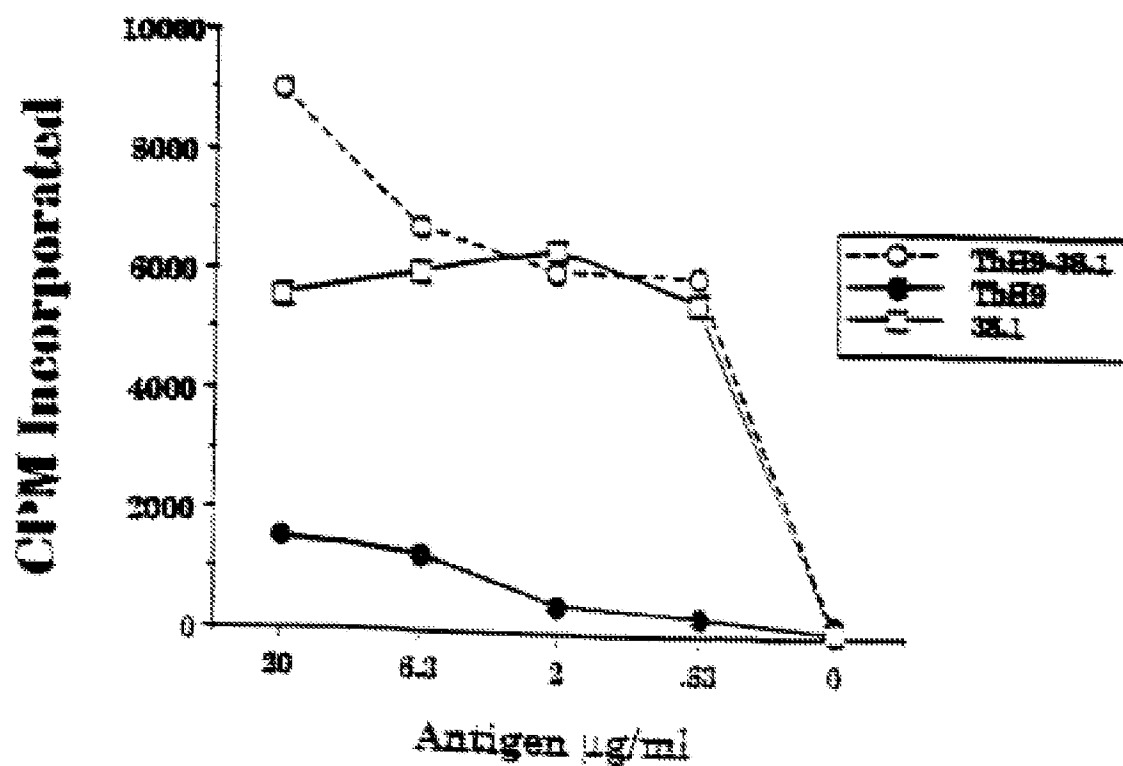


D131 IFN γ

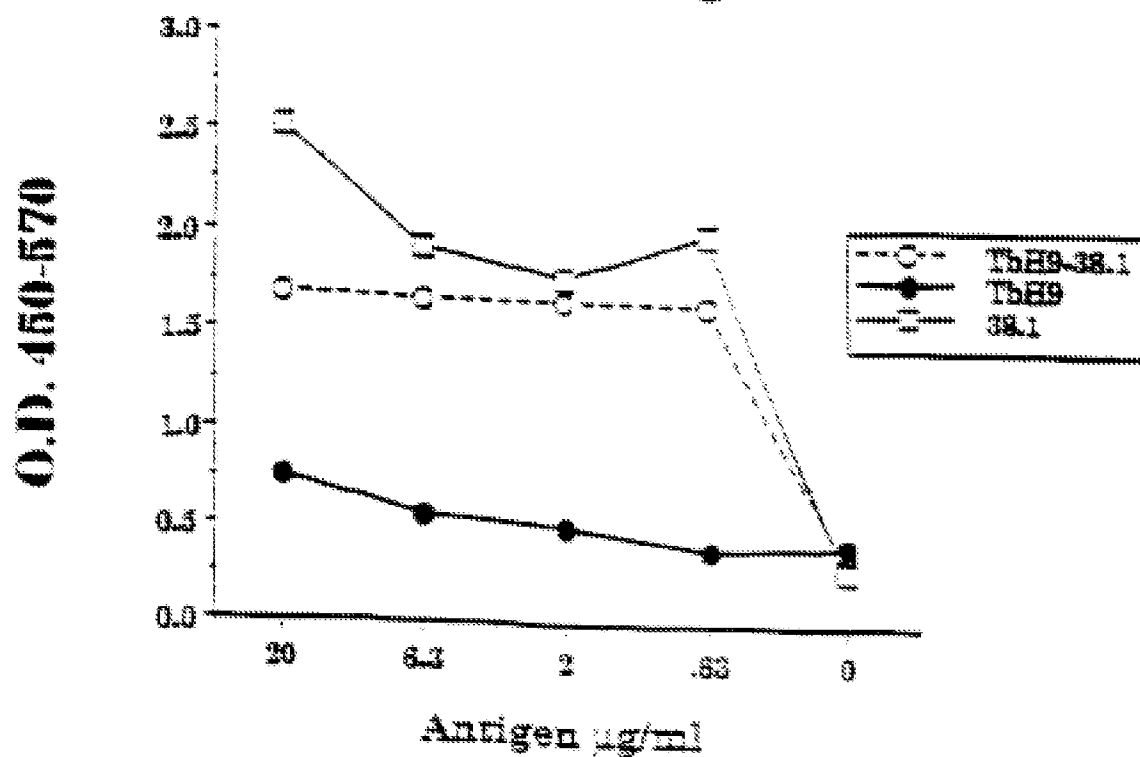


FIGS. 5 A-B

D184 T Cell Proliferation

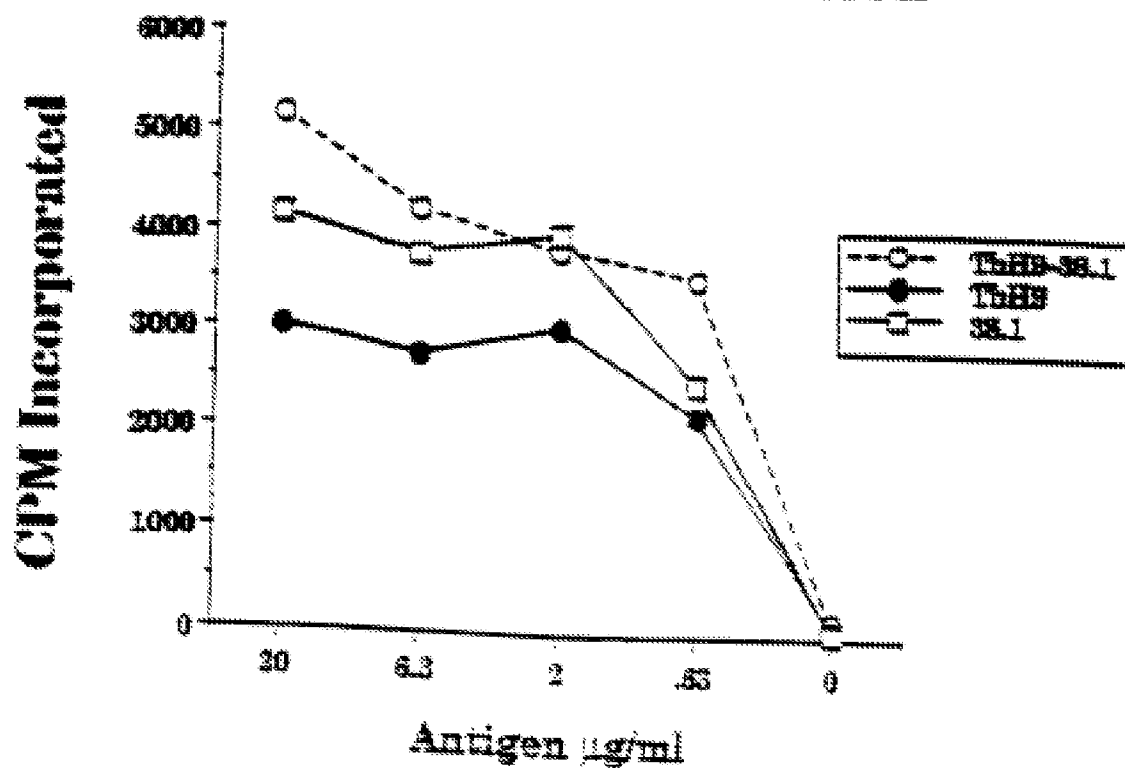


D184 IFN γ

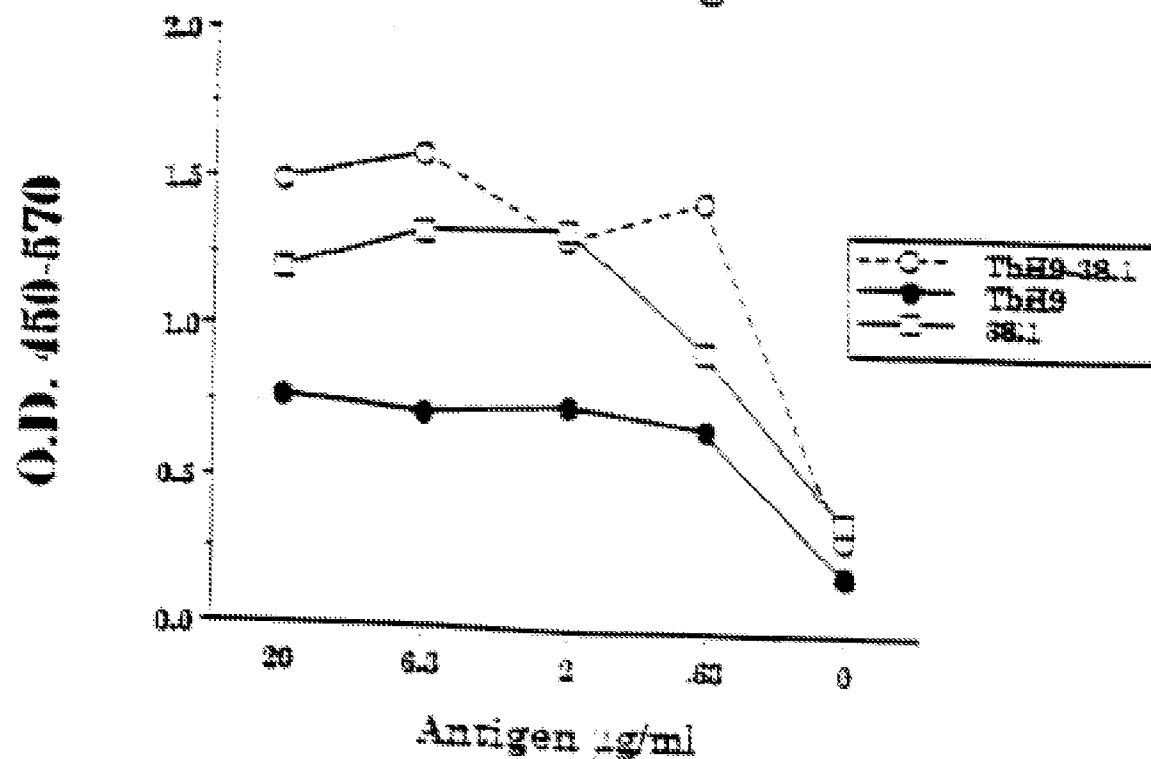


FIGS. 6 A-B

D201 T Cell Proliferation

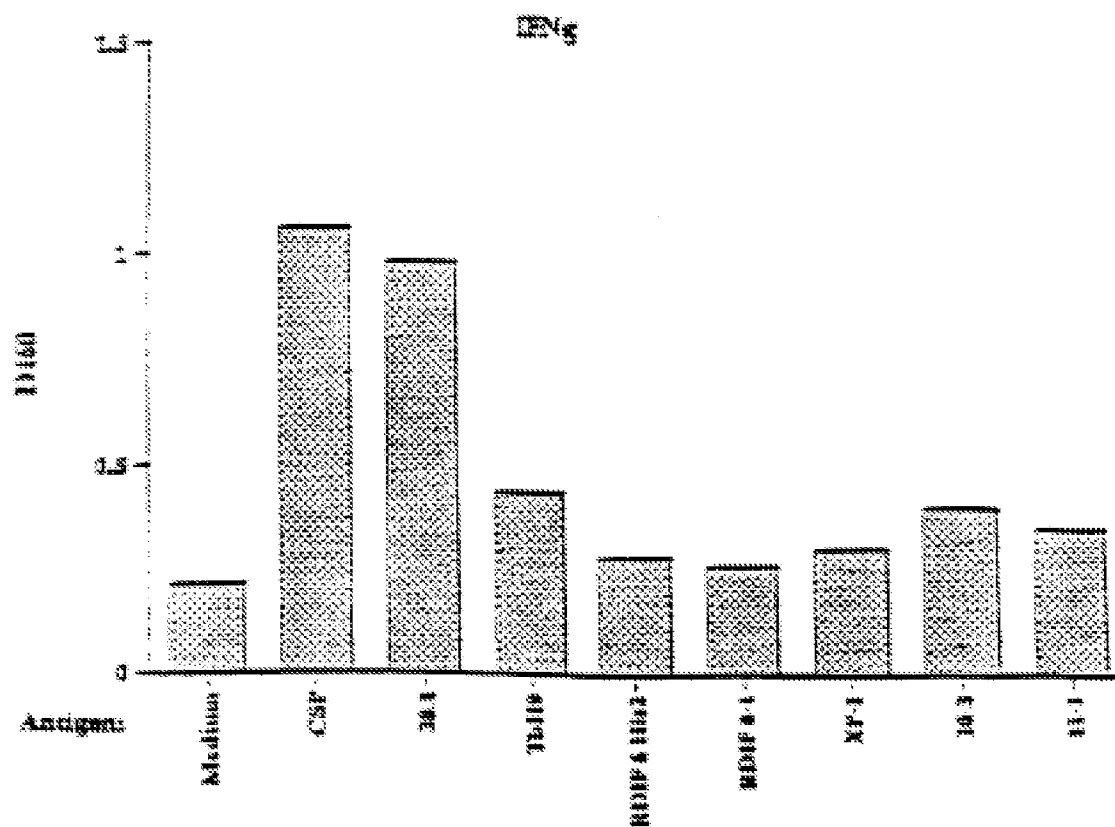
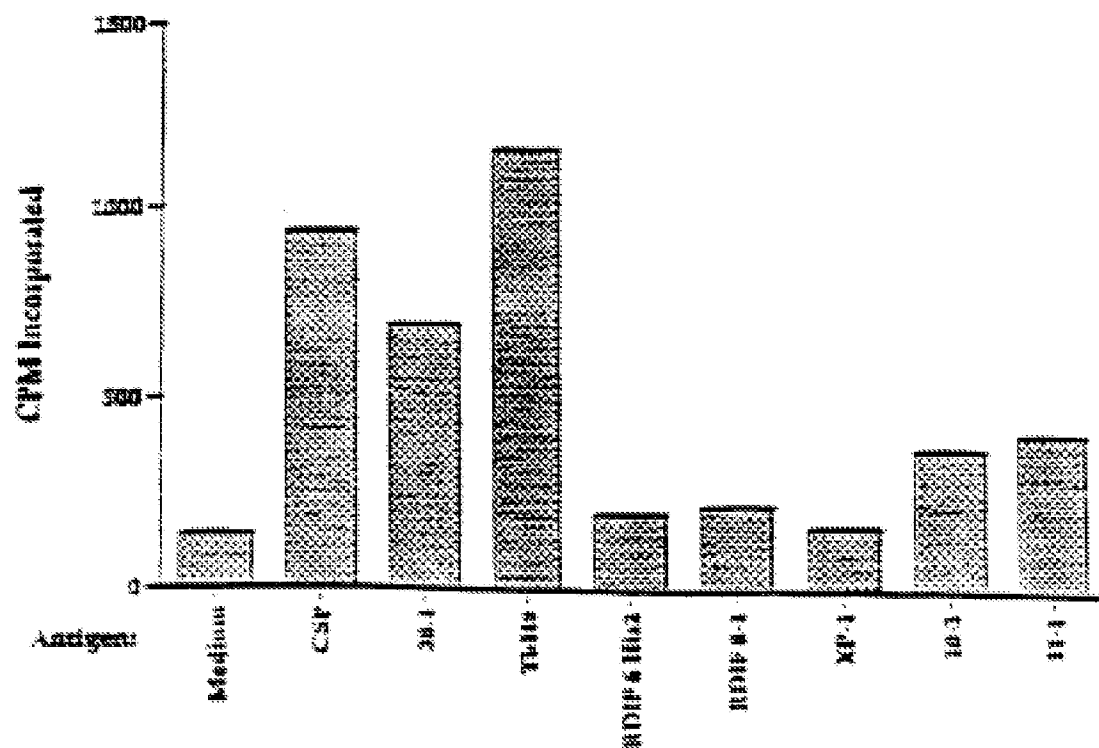


D201 IFN γ

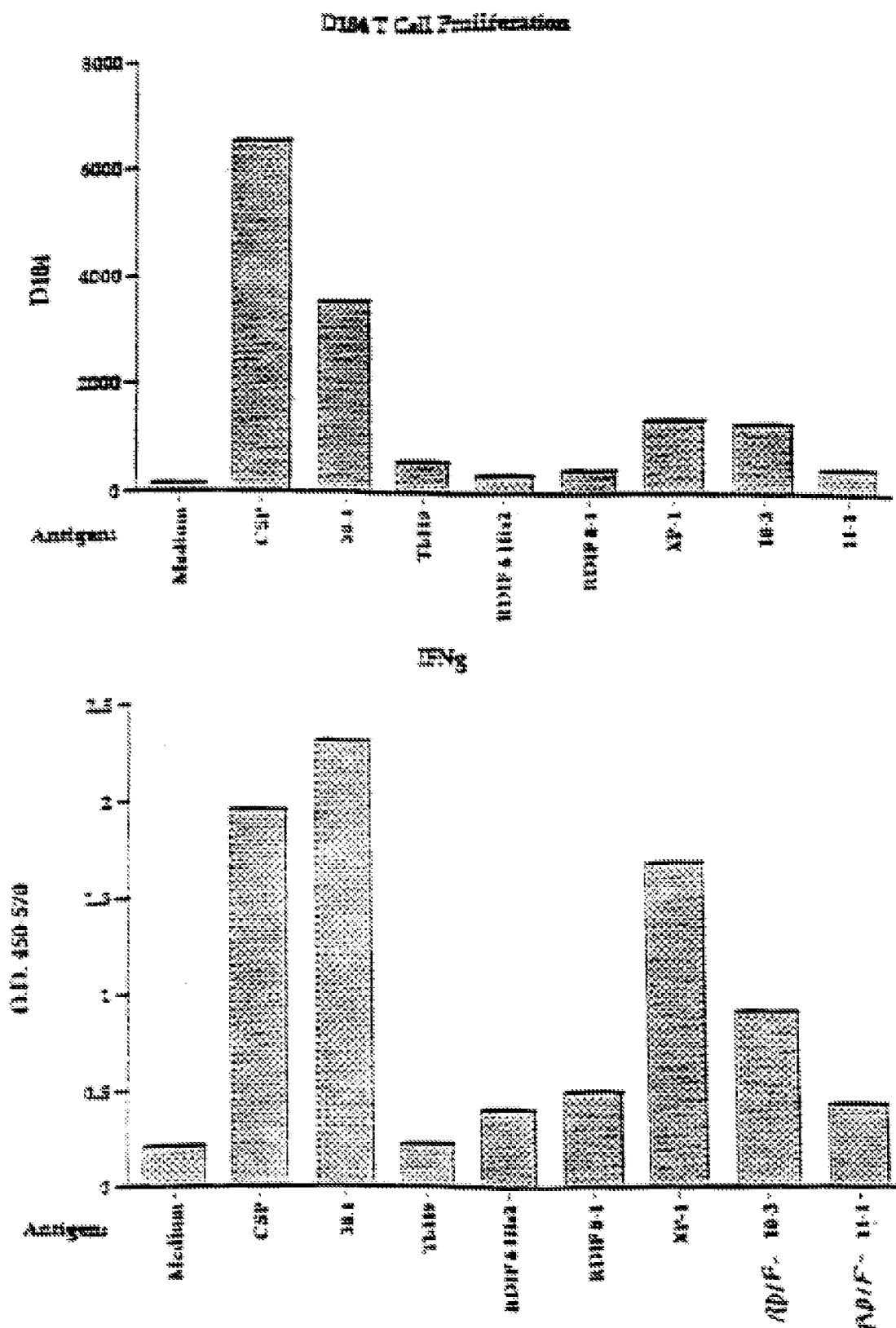


FIGS. 7A-B

D160 T Cell Proliferation



FIGS. 8A-B



FIGS. 9A-B

**Tuberculosis: Protection of Cynomolgus Monkeys
with Recombinant Antigens of Mtb**

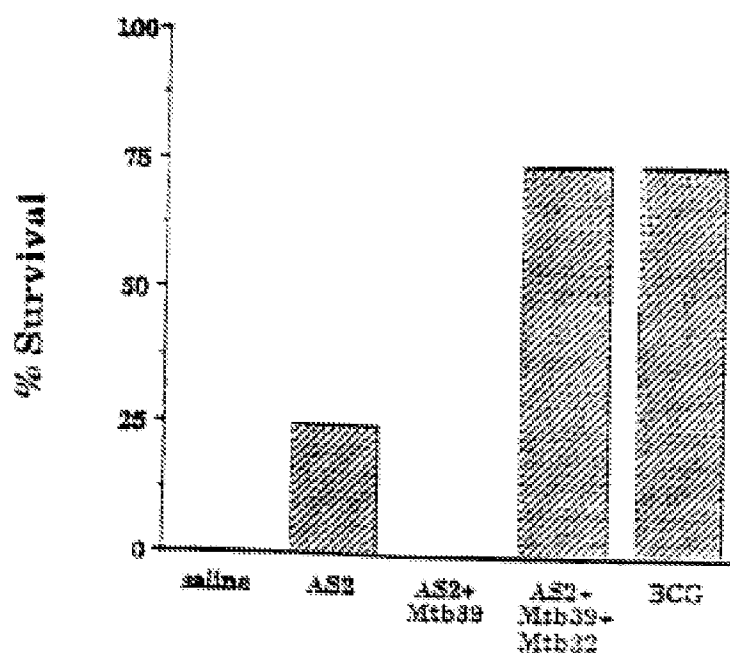
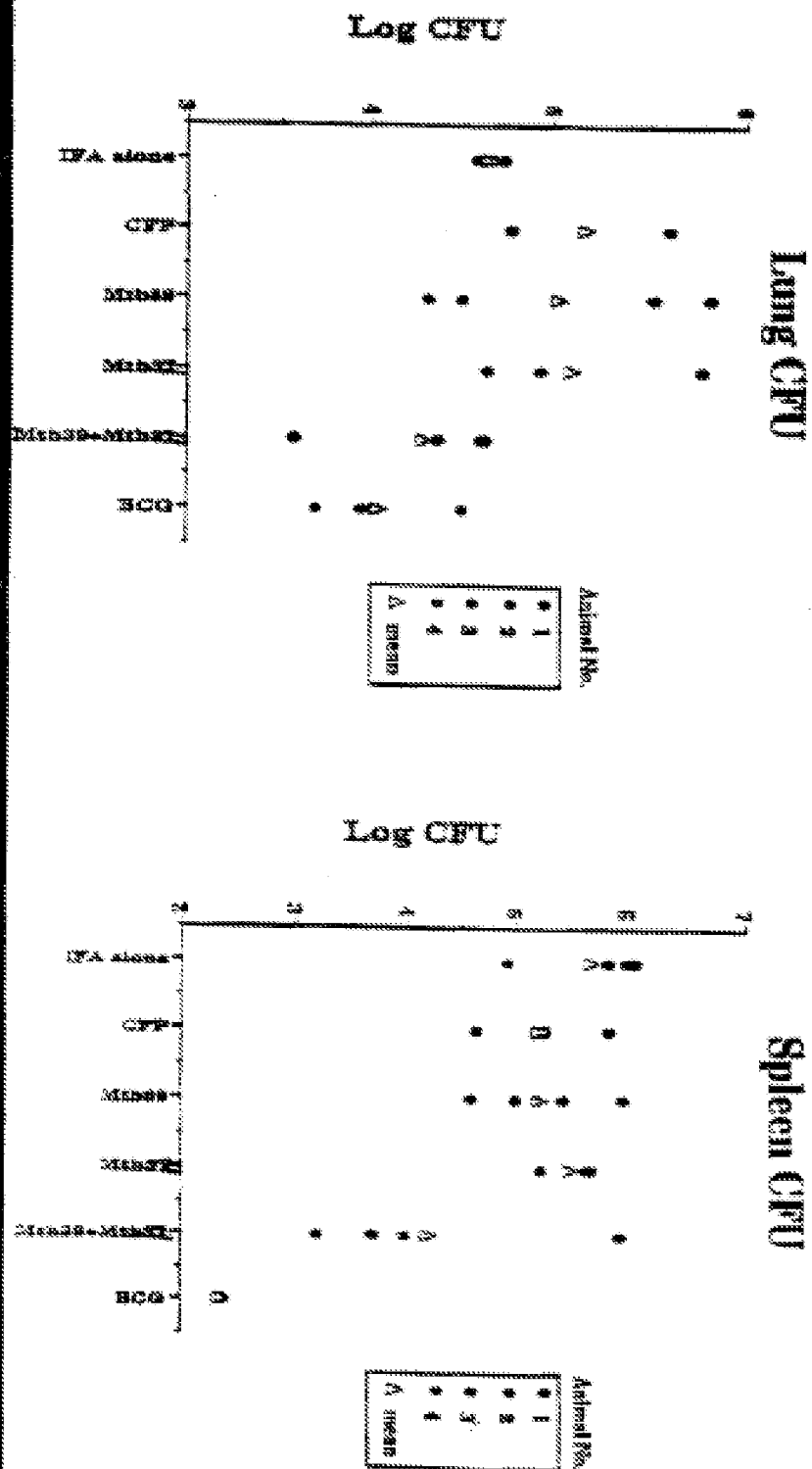


FIG. 10

Aerosol TTB Challenge of Vaccinated Guinea Pigs



FIGS. 11 A-B

DNA Immunized mice challenged with aerosol TB (lung CFU)

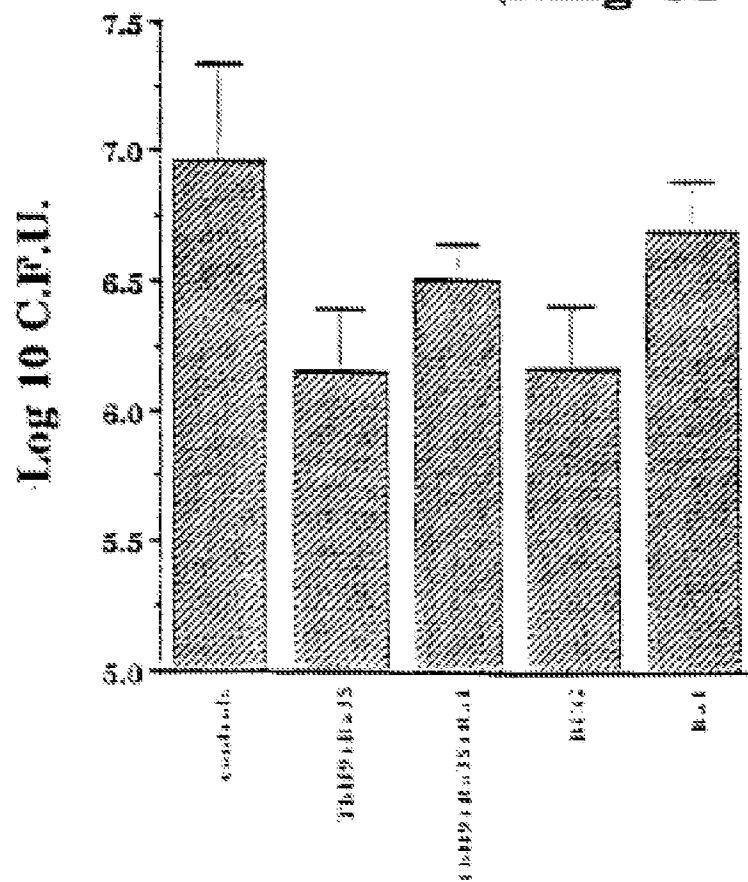


FIG. 12